GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 18:27:02 ; Search time 307 Seconds
(without alignments)
10398.618 Million cell updates/sec

Title: US-09-446-089E-1
Perfect score: 1951
Sequence: 1 aaattacattgcttcctttg.....aataaggattacttttgag 1951

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	471.8	24.2	1989	4	US-09-889-463A-19	Sequence 19, Appl
2	462.2	23.7	2485	4	US-09-889-463A-9	Sequence 9, Appli
3	448.8	23.0	2044	4	US-09-889-463A-27	Sequence 27, Appl
4	440.6	22.6	1990	4	US-08-482-934A-1	Sequence 1, Appli
5	394.8	20.2	2181	4	US-09-443-067-19	Sequence 19, Appl
6	370.4	19.0	2260	4	US-09-889-463A-35	Sequence 35, Appl
7	297	15.2	1522	4	US-09-443-067-25	Sequence 25, Appl
8	287	14.7	1994	4	US-09-889-463A-31	Sequence 31, Appl
9	284	14.6	1993	4	US-09-889-463A-13	Sequence 13, Appl
10	264.8	13.6	852	4	US-09-889-463A-15	Sequence 15, Appl
11	260.2	13.3	671	3	US-09-129-030-29	Sequence 29, Appl
12	258.8	13.3	2057	4	US-09-443-067-29	Sequence 29, Appl
13	257.8	13.2	988	4	US-09-889-463A-25	Sequence 25, Appl
14	249.4	12.8	662	3	US-09-129-030-35	Sequence 35, Appl
15	233	11.9	590	3	US-09-129-030-11	Sequence 11, Appl
16	233	11.9	670	4	US-09-443-067-15	Sequence 15, Appl
17	232	11.9	2145	3	US-09-078-862-1	Sequence 1, Appli
18	232	11.9	2146	4	US-09-866-153-11	Sequence 11, Appl
19	232	11.9	2146	4	US-09-693-467A-11	Sequence 11, Appl
20	232	11.9	2146	4	US-09-270-976-11	Sequence 11, Appl
21	230.2	11.8	1761	3	US-08-481-190-1	Sequence 1, Appli
22	230.2	11.8	1761	5	PCT-US93-00869-1	Sequence 1, Appli
23	225.4	11.6	588	3	US-09-129-030-27	Sequence 27, Appl
24	222.4	11.4	1764	3	US-08-481-190-14	Sequence 14, Appl
25	222.4	11.4	1764	5	PCT-US93-00869-14	Sequence 14, Appl
26	221	11.3	689	3	US-09-129-030-33	Sequence 33, Appl
27	219.6	11.3	1749	3	US-08-481-190-17	Sequence 17, Appl
28	219.6	11.3	1749	5	PCT-US93-00869-17	Sequence 17, Appl
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31	211	10.8	1788	3	US-08-481-190-5	Sequence 5, Appli
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33	209	10.7	590	3	US-09-129-030-13	Sequence 13, Appl
34	208.6	10.7	875	4	US-09-443-067-27	Sequence 27, Appl
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36	194.8	10.0	1315	4	US-08-482-934A-11	Sequence 11, Appl
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38	188.2	9.6	667	3	US-09-129-030-25	Sequence 25, Appl
39	188.2	9.6	668	3	US-09-129-030-31	Sequence 31, Appl
40	188	9.6	2028	4	US-09-889-463A-33	Sequence 33, Appl
41	185.6	9.5	960	4	US-09-443-067-7	Sequence 7, Appli
42	174.8	9.0	527	3	US-09-129-030-3	Sequence 3, Appli
43	172	8.8	1325	4	US-08-482-934A-9	Sequence 9, Appli
44	165.8	8.5	674	3	US-09-129-030-23	Sequence 23, Appl
45	165.2	8.5	512	3	US-09-129-030-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-889-463A-19
; Sequence 19, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-19

Query Match 24.2%; Score 471.8; DB 4; Length 1989;
Best Local Similarity 59.7%; Pred. No. 2.1e-134;
Matches 929; Conservative 0; Mismatches 577; Indels 51; Gaps 6;

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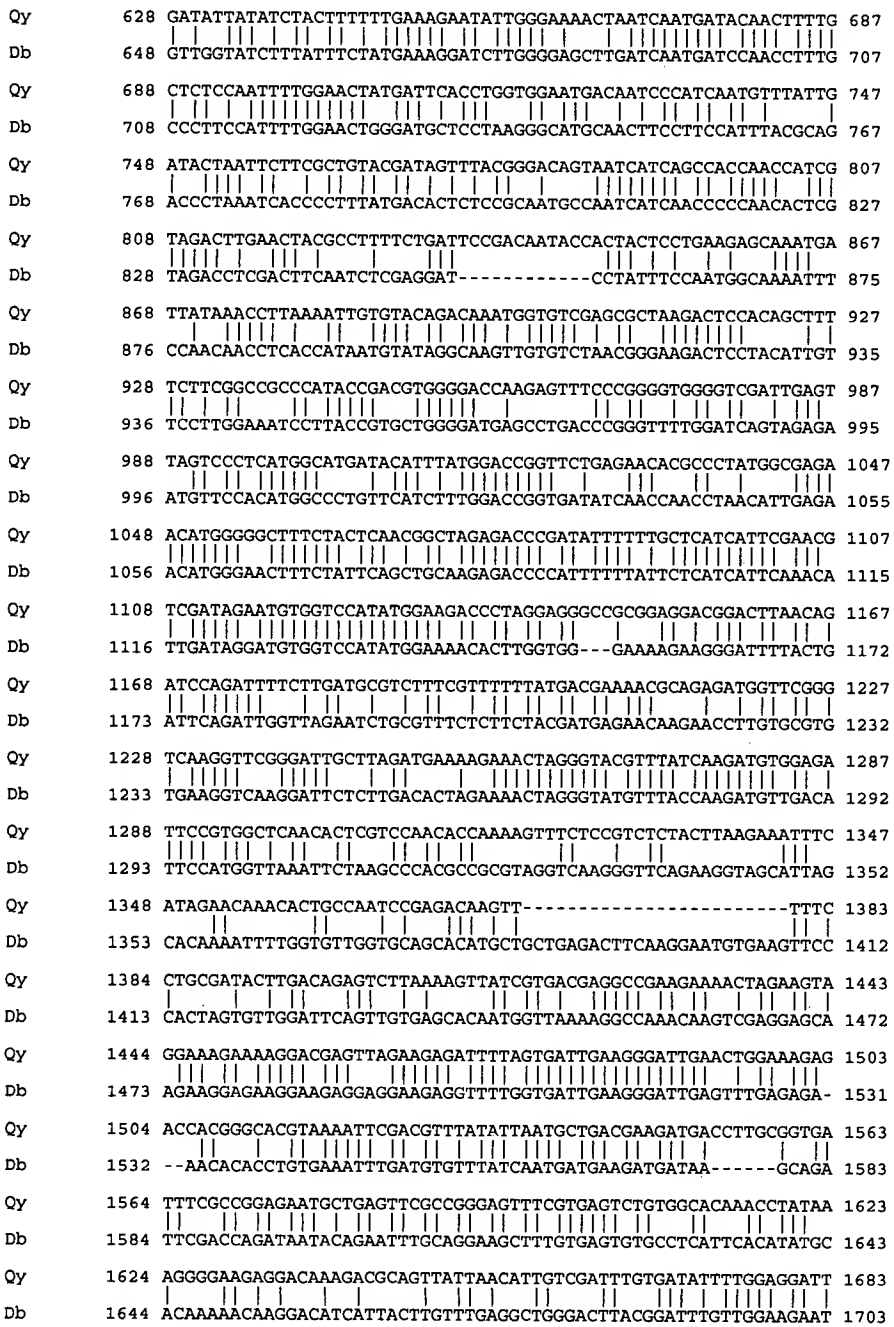
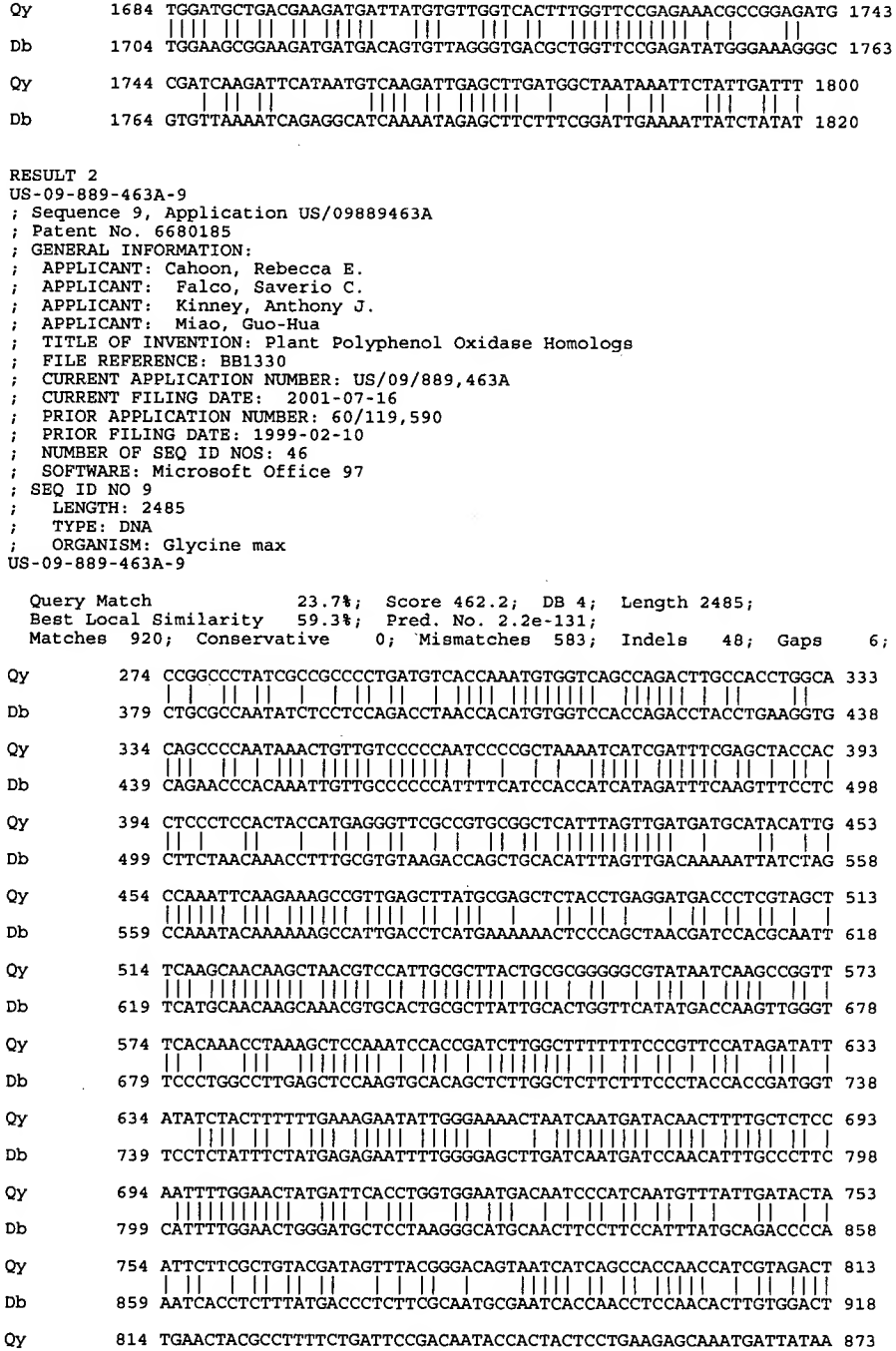
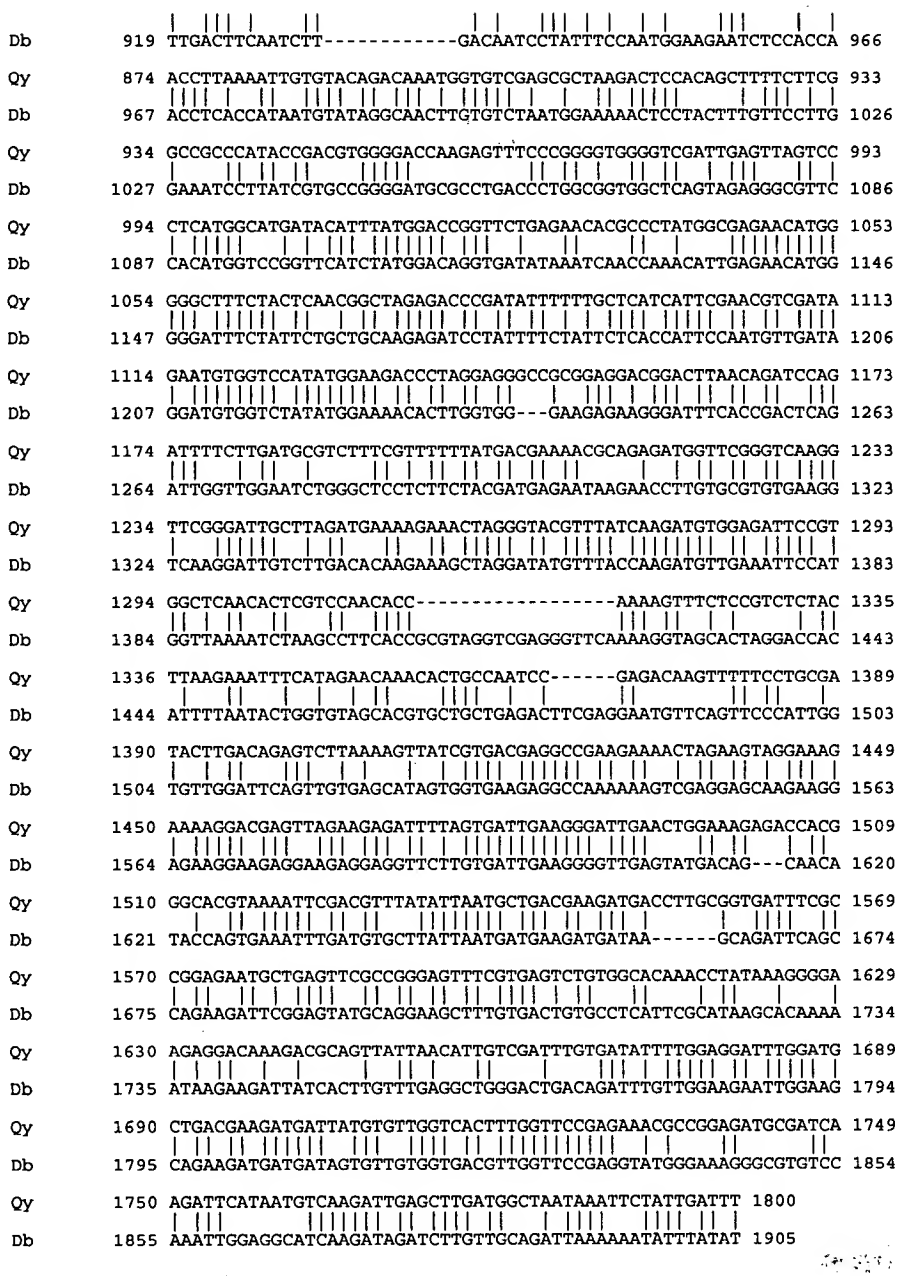




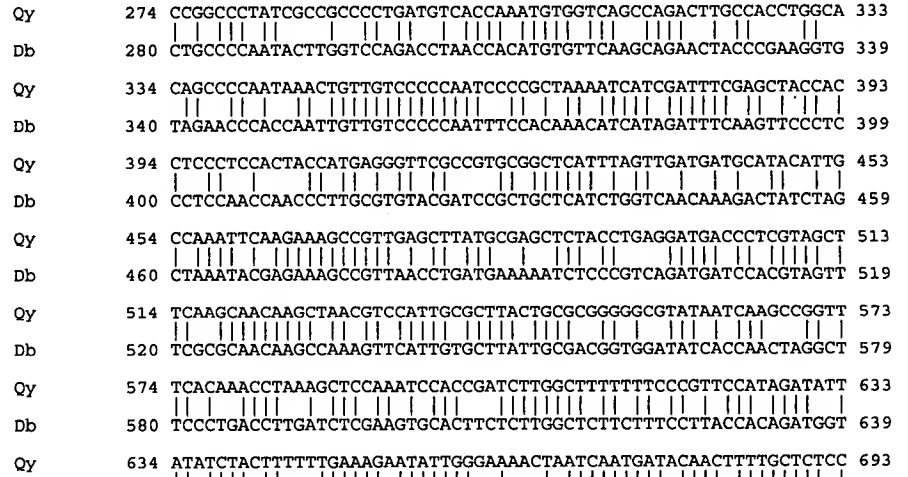
RESULT 2
US-09-889-463A-9
; Sequence 9, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 2485
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-9

Query Match 23.7%; Score 462.2; DB 4; Length 2485;
Best Local Similarity 59.3%; Pred. No. 2.2e-131;
Matches 920; Conservative 0; Mismatches 583; Indels 48; Gaps 6;



RESULT 3
US-09-889-463A-27
; Sequence 27, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 2044
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-27

Query Match 23.0%; Score 448.8; DB 4; Length 2044;
Best Local Similarity 58.8%; Pred. No. 2.7e-127;
Matches 918; Conservative 0; Mismatches 587; Indels 57; Gaps 6;



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Qy       1801 CT 1802
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Db       1816 AT 1817
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RESULT 4
US-08-482-934A-1
; Sequence 1, Application US/08482934A
; Patent No. 6703542
;  GENERAL INFORMATION:
;    APPLICANT:  Robinson, Simon P.
;    APPLICANT:  Dry, Ian B.
;    TITLE OF INVENTION:  Polyphenol Oxidase Genes
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,934A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/182,045
;      FILING DATE:  14-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/AU92/00356
;      FILING DATE:  16-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PK7248
;      FILING DATE:  17-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John P. White
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  51461-Z/JPW/GJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  GPO1 cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..1848
US-08-482-934A-1

  Query Match             22.6%;  Score 440.6;  DB 4;  Length 1990;
  Best Local Similarity   57.9%;  Pred. No. 8.8e-125;
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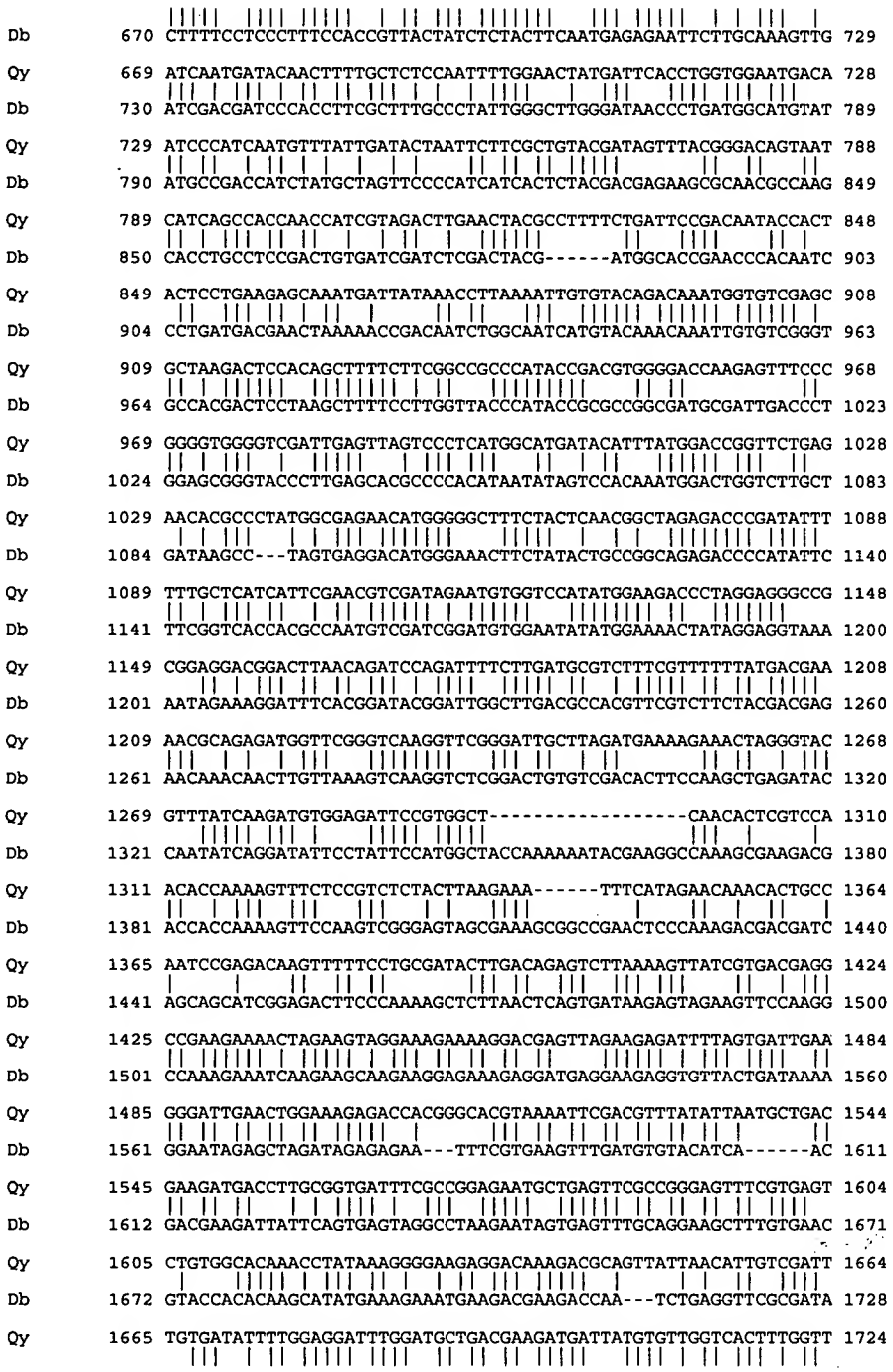

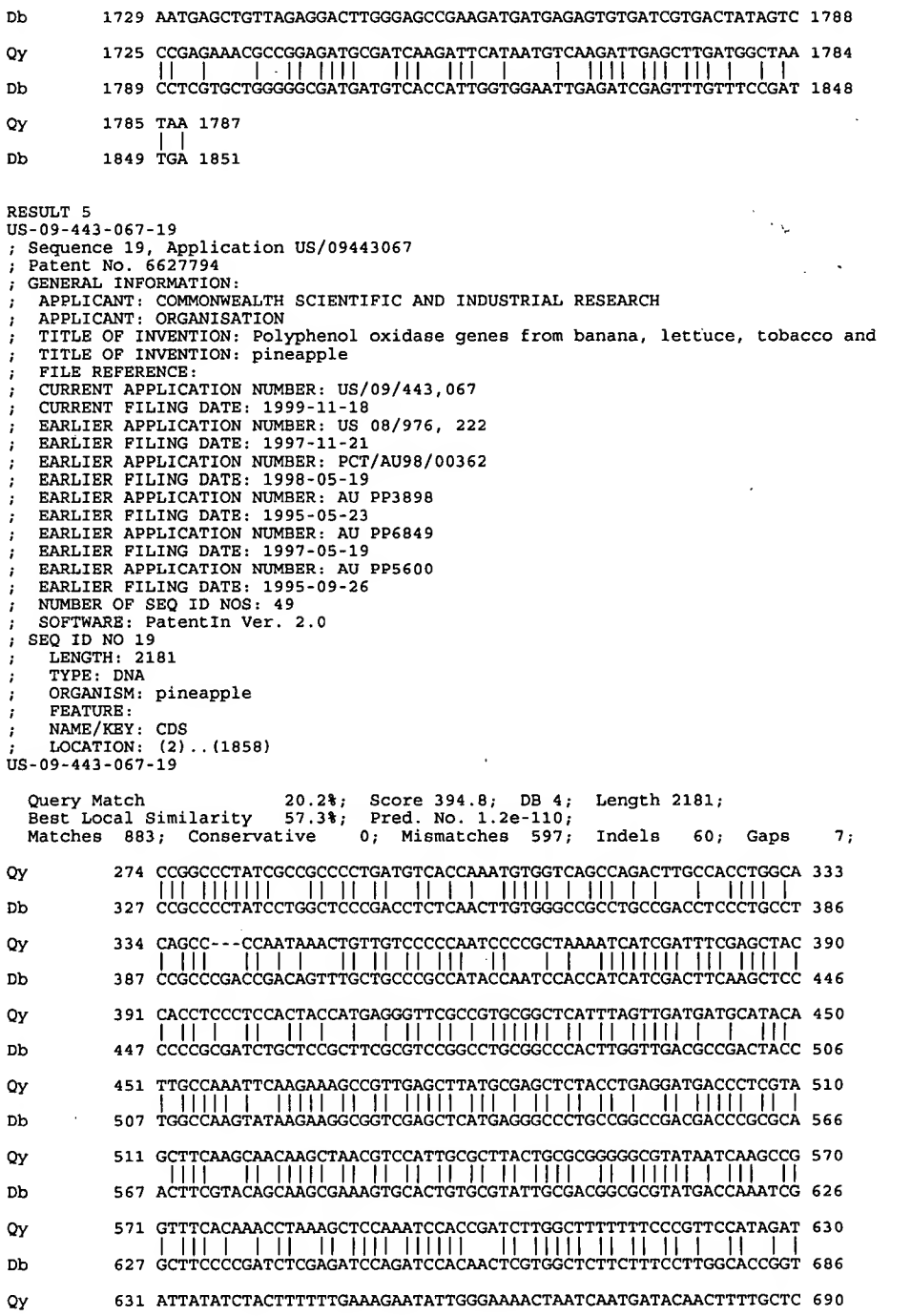

RESULT 5
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; Sequence 19, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976, 222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: pineapple
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1858)
US-09-443-067-19

Query Match 20.2%; Score 394.8; DB 4; Length 2181;
Best Local Similarity 57.3%; Pred. No. 1.2e-110;
Matches 883; Conservative 0; Mismatches 597; Indels 60; Gaps 7;

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Db       1218 CCGACTGGCTCAACGCGTCCTTCCTGTTCTATGATGAGAATGCGCAGCTCGTCCGTGTTA 1277

Qy       1231 AGGTTCGGGATTGCTTAGATGAAAAGAAACTAGGGTACGTTTATCAAGATGTGGAGATTC 1290

Db       1278 AAGTAAAAGACTGCTTAGAGGCCGACGCAATGCGGTACACATACCAGGATGTAGAGATCC 1337

Qy       1291 CGTGGCTCAACACTCGTCCAACACCAAAAGTTTCTC---------------------- 1326

Db       1338 CGTGGCTCAAAGCAAAGCCGACGCCAAAGAGCGCCCTACAGAAGATAAAGAGCAAGGTAT 1397

Qy       1327 CGTCTCTACTTAAGAAATTTCATAGAACAAACACTGCCAATCCGAGACAAGTTTTTCCTG 1386

Db       1398 CGACGCTGAAGGCAACACCAAGGGGGACGACGACTACCACAGCAGAGACTACATTTCCGG 1457

Qy       1387 CGATACTTGACAGAGTCTTAAAAGTTATCGTGACGAGGCCGAAGAAAACTAGAAGTAGGA 1446

Db       1458 TGGTGCTGGATAAGCCGGTGAGTGCAACAGTGGCTAGACCGAAGGCCAGGAGGAGTGGGA 1517

Qy       1447 AAGAAAAGGACGAGTTAGAAGAGATTTTAGTGATTGAAGGGATTGAACTGGAAAGAGACC 1506

Db       1518 AGGAGAAGGAAGAAGAGGAGGAGGTGTTGGTGGTGGAGGGAATCGAGTTGGAGAAGG--- 1574

Qy       1507 ACGGGCACGTAAAATTCGACGTTTATATTAATGCTGACGAAGATGACCTTGCGGTGATTT 1566

Db       1575 ACGTGTTCGTGAAGTTTGATGTGTATATAAACTCGCCGGAGCACGAAGGGGTGGG----- 1629

Qy       1567 CGCCGGAGAATGCTGAGTTCGCCGGGAGTTTCGTGAGTCTGTGGCACAAACCTATAAAGG 1626

Db       1630 -GCCGGAGGCGAGTGAGTTCGCAGGGAGCTTCGTCCACGTGCCACACAAGCACAAGAAGG 1688

Qy       1627 GGAAGAGGACAAAGACGCAGTTAT---------------TAACATTGTCGATTTGTGATA 1671

Db       1689 CGAAGAAGGGGAAGGAGATGGCCAGGATGAACACAAGGCTTAAGCTCGGGATAACGGACC 1748

Qy       1672 TTTTGGAGGATTTGGATGCTGACGAAGATGATTATGTGTTGGTCACTTTGGTTCCGAGAA 1731

Db       1749 TGCTCGAGGACATCGGCGCTGAGGACGACGAGAGCGTGCTCATCACGCTCGTGCCCAGGA 1808

Qy       1732 ACGCCGGAGATGCGATCAAGATTCATAATGTCAAGATTGA 1771

Db       1809 GCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTGA 1848
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RESULT 6
US-09-889-463A-35
; Sequence 35, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 2260
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-35

Query Match 19.0%; Score 370.4; DB 4; Length 2260;
Best Local Similarity 56.3%; Pred. No. 4.2e-103;
Matches 808; Conservative 0; Mismatches 601; Indels 27; Gaps 5;

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Qy        357 CCAATCCCCGCTAAAATCATCGATTTC---GAGCTACCACCTCCCTCCACTACCATGAGG 413

Db        463 CCACCTCCTTCTAAGATCATAGATTTCAAAGATTTTGCTTCTCCAAACGCCACGCTTCGA 522

Qy        414 GTTCGCCGTGCGGCTCATTTAGTTGATGATGCATACATTGCCAAATTCAAGAAAGCCGTT 473

Db        523 GTAAGAAAACCGGCTCACATGGTAGATGAGGAGTACATAGCAAAACTTGAAAAGGGCATT 582

Qy        474 GAGCTTATGCGAGCTCTACCTGAGGATGACCCTCGTAGCTTCAAGCAACAAGCTAACGTC 533

Db        583 GCACTCATGAAAGCACTCCCTGATGATGACCCACGTAATTTCATACAACAAGCAAAGGTC 642

Qy        534 CATTGCGCTTACTGCGCGGGGGCGTATAATCAAGCCGGT---TTCACAAACCTAAAGCTC 590

Db        643 CATTGTGCTTATTGTAACGGTGCCTATCACCTACCCCATCCCTTTCAGAACACAAAACTC 702

Qy        591 CAAATCCACCGATCTTGGCTTTTTTTCCCGTTCCATAGATATTATATCTACTTTTTTGAA 650

Db        703 AACATTCACAGGTCTTGGTTTTTCTTTCCTTTCCACCGTTGGTACATTTACTTCTTCGAG 762

Qy        651 AGAATATTGGGAAAACTAATCAATGATACAACTTTTGCTCTCCAATTTTGGAACTATGAT 710

Db        763 CGAATCTTGGGAAGCTTGCTCGGTGACCCGAACTTTGCCTTACCGTTTTGGAATTGGGAT 822

Qy        711 TCACCTGGTGGAATGACAATCCCATCAATGTTTATTGATACTAATTCTTCGCTGTACGAT 770

Db        823 GCTGTAGAAGGGATGCAAATGCCACCATATTTCGCAAACCCTAACTCGTCGCTCTATCAC 882

Qy        771 AGTTTACGGGACAGTAATCATCAGCCACCAACCATCGTAGACTTGAACTACGCCTTTTCT 830

Db        883 AAACTCCGAAACCCCAAGCACTTGCCACCGCAAGTGGTTGACCTGAACTATGATCCATTT 942

Qy        831 GATTCCGACAATACCACTACTCCTGAAGAGCAAATGATTATAAACCTTAAAATTGTGTAC 890

Db        943 GACTTTAATGATGATACACCTTCTCATCAACAAGTTTCGTATAATCTAGCCTTCATGTAC 1002

Qy        891 AGACAAATGGTGTCGAGCGCTAAGACTCCACAGCTTTTCTTCGGCCGCCCATACCGACGT 950

Db       1003 AAGCAAATGGT---GCTAGCAAGTACCAAAGAATTGTTCATGGGAAGCCCTTTTCGACTC 1059
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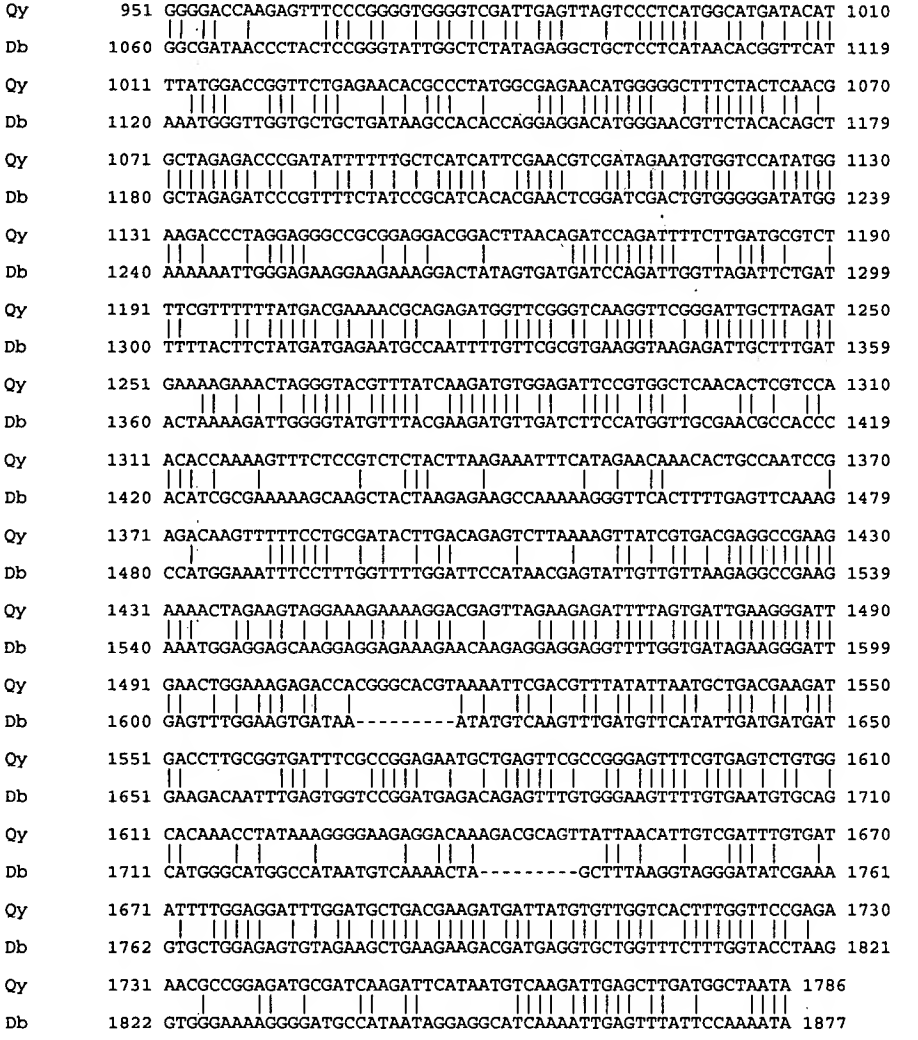
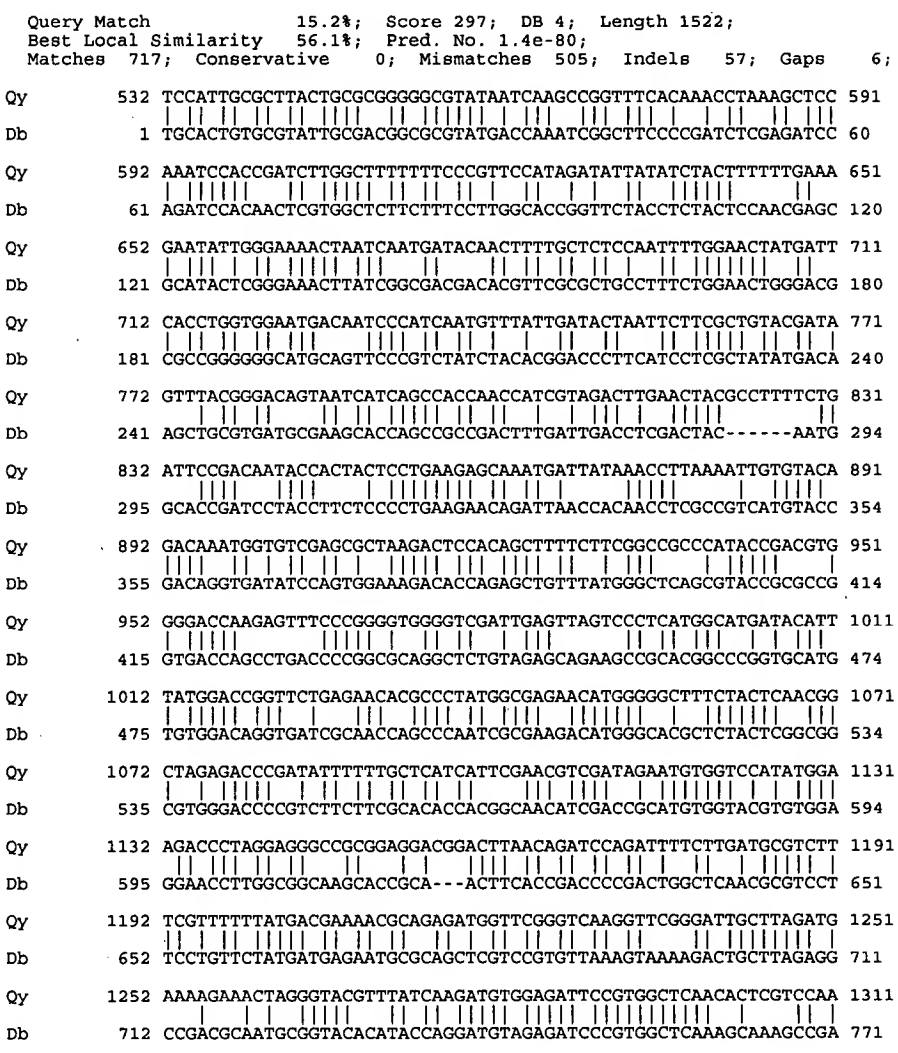
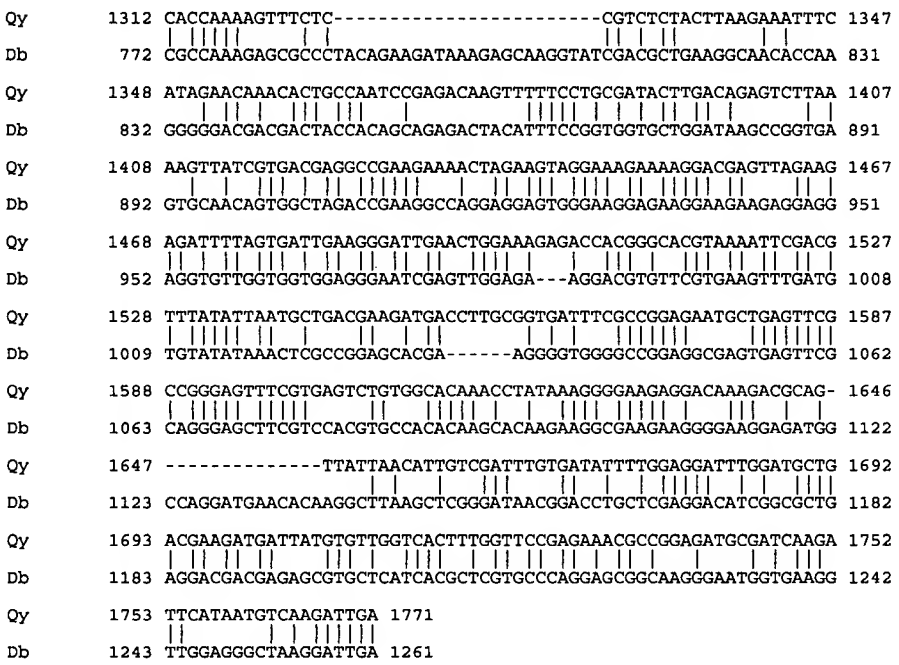


RESULT 7
US-09-443-067-25
; Sequence 25, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976, 222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: pineapple
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1271)
US-09-443-067-25

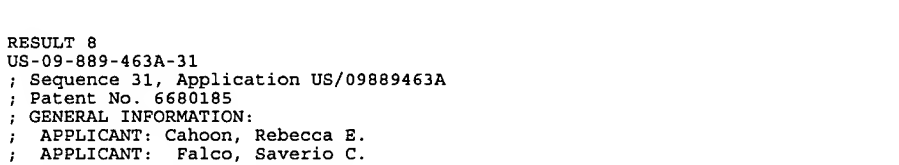
Query Match 15.2%; Score 297; DB 4; Length 1522;
Best Local Similarity 56.1%; Pred. No. 1.4e-80;
Matches 717; Conservative 0; Mismatches 505; Indels 57; Gaps 6;

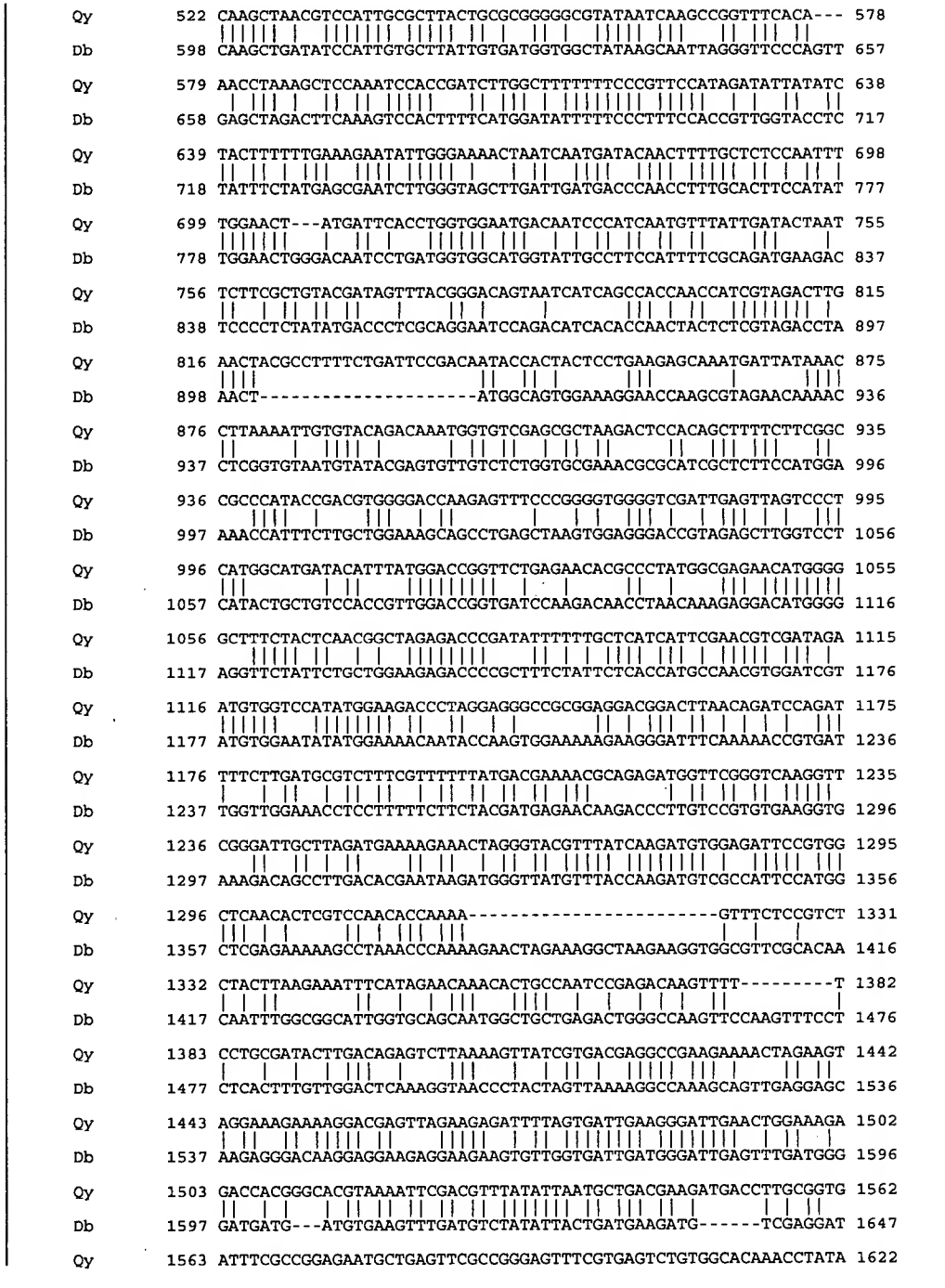


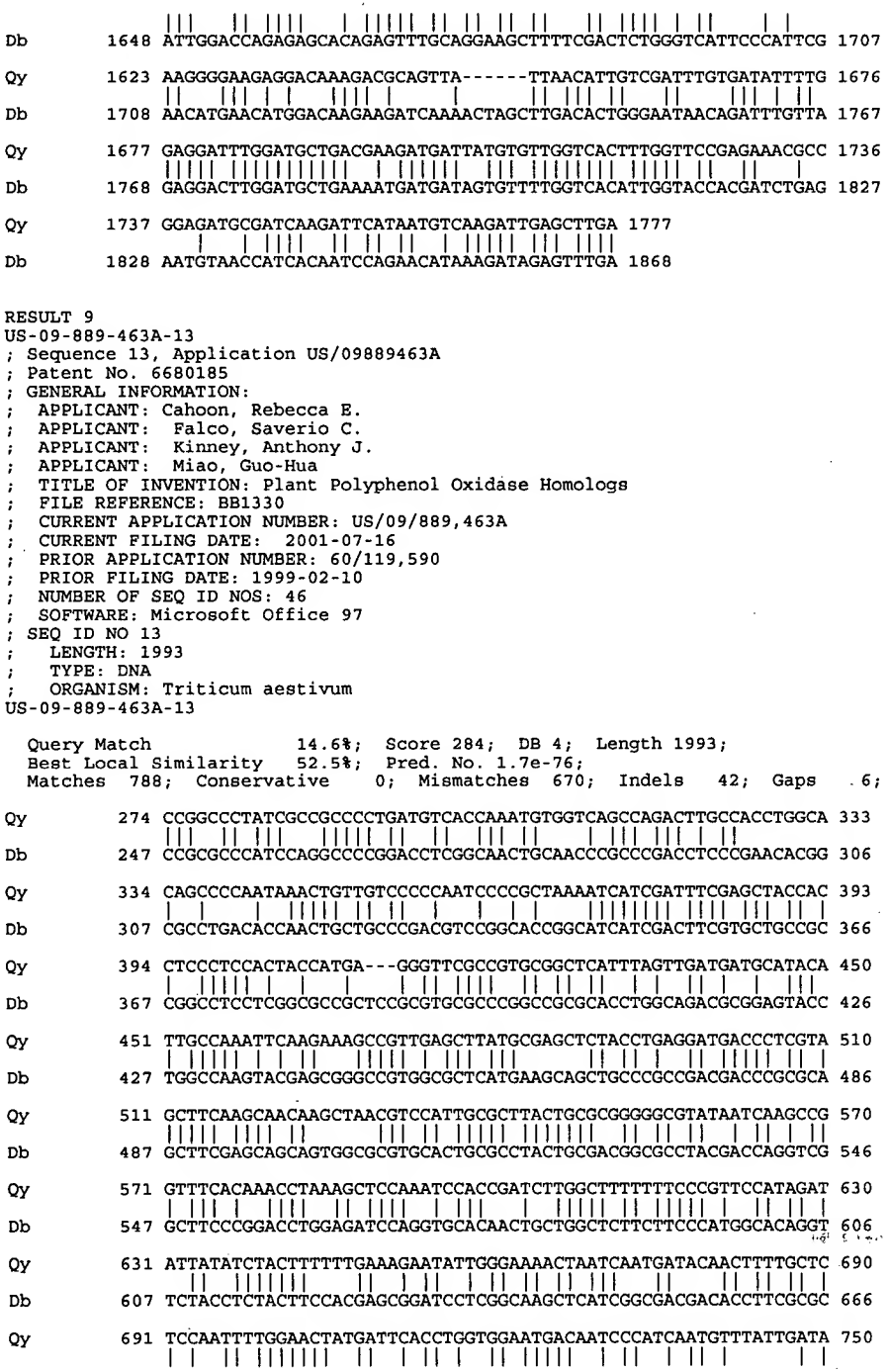


RESULT 8
US-09-889-463A-31
; Sequence 31, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-31

Query Match 14.7%; Score 287; DB 4; Length 1994;
Best Local Similarity 55.0%; Pred. No. 2e-77;
Matches 781; Conservative 0; Mismatches 565; Indels 75; Gaps 8;







RESULT 10
US-09-889-463A-15

; Sequence 15, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (515)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (543)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (668)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (718)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (720)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (722)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (737)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (746)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (791)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (799)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (823)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (841)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (848)
; OTHER INFORMATION: n = a, c, g or t
US-09-889-463A-15

Query Match 13.6%; Score 264.8; DB 4; Length 852;
Best Local Similarity 63.9%; Pred. No. 8.1e-71;
Matches 420; Conservative 0; Mismatches 225; Indels 12; Gaps 1;

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Qy        498 GATGACCCTCGTAGCTTCAAGCAACAAGCTAACGTCCATTGCGCTTACTGCGCGGGGGCG 557
              ||||||| ||||  ||||  |||||||| ||||| ||||| ||||| || |  || ||
Db          8 GATGACCCGCGTAATTTCACCCAACAAGCCAACGTTCATTGTGCTTATTGTGATGGTGCA 67

Qy        558 TATAATCAAGCCGGTTTCACAAACCTAAAGCTCCAAATCCACCGATCTTGGCTTTTTTTC 617
              ||| | ||||  || ||| |  ||||  | ||||| ||||   || ||||| || |||
Db         68 TATCACCAAGTTGGGTTCCCTGACCTCGATCTCCAAGTCCACAACTCCTGGCTCTTCTTC 127

Qy        618 CCGTTCCATAGATATTATATCTACTTTTTTGAAAGAATATTGGGAAAACTAATCAATGAT 677
              || |||||| | |  ||| | || || | |||||| || ||||| |   | |||||||||
Db        128 CCTTTCCATCGTTGGTATCTTTATTTCTATGAAAGGATCTTGGGGAGCTTGATCAATGAT 187

Qy        678 ACAACTTTTGCTCTCCAATTTTGGAACTATGATTCACCTGGTGGAATGACAATCCCATCA 737
              |||| ||||| || | ||||||||||  ||| | |||   || |||  | | || ||
Db        188 CCAACCTTTGCCCTTCCATTTTGGAACTGGGATGCTCCTAAGGGCATGCAACTTCCTTCC 247

Qy        738 ATGTTTATTGATACTAATTCTTCGCTGTACGATAGTTTACGGGACAGTAATCATCAGCCA 797
              || |     ||  |||| ||  | || || || | | | ||  |    |||||||| ||
Db        248 ATTTACGCAGACCCTAAATCACCCCTTTATGACACTCTCCGCAATGCCAATCATCAACCC 307

Qy        798 CCAACCATCGTAGACTTGAACTACGCCTTTTCTGATTCCGACAATACCACTACTCCTGAA 857
              |||||  |||||||| |  ||| |    |   |||                ||| | |  |
Db        308 CCAACACTCGTAGACCTCGACTTCAATCTCGAGGAT------------CCTATTTCCAAT 355

Qy        858 GAGCAAATGATTATAAACCTTAAAATTGTGTACAGACAAATGGTGTCGAGCGCTAAGACT 917
              |   ||||    |  ||||| |  ||  |||| |  ||| | ||||| | ||  ||||||
Db        356 GGCAAAATTTCCAACAACCTCACCATAATGTATANGCAAGTTGTGTCTAACGGGAAGACT 415

Qy        918 CCACAGCTTTTCTTCGGCCGCCCATACCGACGTGGGGACCAAGAGTTTCCCGGGGTGGGG 977
              ||     | ||| | ||    || |||||   ||||||  |       || |||  | ||
Db        416 CCTACATTGTTCCTTGGAAATCCTTACCGTGCTGGGGATGAGCCTGACCCGGGTTTTGGA 475

Qy        978 TCGATTGAGTTAGTCCCTCATGGCATGATACATTTATGGACCGGTTCTGAGAACACGCCC 1037
              ||  | |||   || || ||||||    | ||| | ||| |||||  |   |||   ||
Db        476 TCAGTAGAGAATGTTCCACATGGCCCTGTTCATCTTTGGNCCGGTGATATCAACCAACCT 535

Qy       1038 TATGGCGAGAACATGGGGGCTTTCTACTCAACGGCTAGAGACCCGATATTTTTTGCTCAT 1097
              |   | |||||||||  ||||||| ||| | ||  ||||||| || |||| | |||||
Db        536 AACATTGNGAACATGGGAACTTTCTATTCAGCTGCAGGAGACCCCATTTTTTATTCTCAT 595

Qy       1098 CATTCGAACGTCGATAGAATGTGGTCCATATGGAAGACCCTAGGAGGGCCGCGGAGG 1154
              ||||| || | ||||  |||||||||||||||| || ||  | |||    | |||
Db        596 CATTCAGACATTGATAAGATGTGGTCCATATGGAAAACACTTTGTGGGAAAAGAAGG 652
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RESULT 11
US-09-129-030-29
; Sequence 29, Application US/09129030A
; Patent No. 6242221
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
; TITLE OF INVENTION: GENOMIC PPO CLONES
; FILE REFERENCE: 57072-PCT-US
; CURRENT APPLICATION NUMBER: US/09/129,030A
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: AU PN7856
; EARLIER FILING DATE: 1996-02-05
; EARLIER APPLICATION NUMBER: AU PO2361
; EARLIER FILING DATE: 1996-09-16
; EARLIER APPLICATION NUMBER: PCT/AU97/00041
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 671

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;   TYPE: DNA
;   ORGANISM: LETTUCE
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(669)
US-09-129-030-29

  Query Match            13.3%;  Score 260.2;  DB 3;  Length 671;
  Best Local Similarity  63.6%;  Pred. No. 1.8e-69;
  Matches  432;  Conservative    0;  Mismatches  238;  Indels    9;  Gaps    2;

Qy        532 TCCATTGCGCTTACTGCGCGGGGGCGTATAATCAAGCCGGTTTCACAAACCTAAAGCTCC 591
              | ||||| || || |||| ||||| ||  |||||| |||||| | | ||  |||| |
Db          2 TGCATTGTGCGTATTGCGATGGGGCATACGATCAAGTCGGTTTCCCTGATCTCGAGCTTC 61

Qy        592 AAATCCACCGATCTTGGCTTTTTTTCCCGTTCCATAGATATTATATCTACTTTTTTGAAA 651
              || ||||  | || ||| | || || || |||||  | |||||  | ||||| || || |
Db         62 AAGTCCATGGCTCATGGTTGTTCTTACCTTTCCACCGCTATTACTTATACTTCTTCGACA 121

Qy        652 GAATATTGGGAAAACTAATCAATGATACAACTTTTGCTCTCCAATTTTGGAACTATGATT 711
              ||| |  ||   | ||||| ||||| ||| ||| ||  |||  |||||||||||  |||
Db        122 AAATTTGTGGCGGATTAATCGATGATCCAAATTTCGCAATCCCTTTTTGGAACTGGGATG 181

Qy        712 CACCTGGTGGAATGACAATCCCATCAATGTTTATTGATACTAATTCTTCGCTGTACGATA 771
              |||||| ||| |||| |||||    || |  |   |||  || ||| || |||||||| |
Db        182 CACCTGATGGCATGAAGATCCCTGATATTTACACGAATAAGAAATCTCCGTTGTACGATG 241

Qy        772 GTTTACGGGACAGTAATCATCAGCCACCAACCATCGTAGACTTGAACTACGCCTTTTCTG 831
              | | || ||    || |||||  |||| |  | | ||  |  |||||       ||
Db        242 CTCTTCGTGATGCGAAGCATCAAGCACCGTCTCTGATTGATCTTGACTAC------AATG 295

Qy        832 ATTCCGACAATACCACTACTCCTGAAGAGCAAATGATTATAAACCTTAAAATTGTGTACA 891
              |  |||  | |    ||  |         ||||     | ||| || | |||| ||||||
Db        296 GTGACGATGAAAATCTTAGCCGATCGAGACAAACCTCCACAAATCTCACAATTATGTACA 355

Qy        892 GACAAATGGTGTCGAGCGCTAAGACTCCACAGCTTTTCTTCGGCCGCCCATACCGACGTG 951
              |||||||||||||| ||  | ||||||  |     |||||| | ||    || || ||   |
Db        356 GACAAATGGTGTCTAGTTCCAAGACTGCTAGTCTTTTCATGGGTACTCCTTATCGTGCAG 415

Qy        952 GGGACCAAGAGTTTCCCGGGGTGGGGTCGATTGAGTTAGTCCCTCATGGCATGATACATT 1011
              | ||  | |     || ||    || ||| | |||    | || ||||||  | | |||
Db        416 GTGATGAGGCTAGCCCTGGCTCTGGCTCGCTCGAGAGCATACCACATGGCCCGGTTCATA 475

Qy       1012 TATGGACCGGTTCTGAGAACACGCCCTATGGCGAGAACATGGGGGCTTTCTACTCAACGG 1071
              | |||||||||    |  ||||  ||   |||| |   |||||||     || || ||  | |
Db        476 TCTGGACCGGAGATAGGAACCAGCAAAATGGTGCAGACATGGGTAACTTTTATTCTGCAG 535

Qy       1072 CTAGAGACCCGATATTTTTTGCTCATCATTCGAACGTCGATAGAATGTGGTCCATATGGA 1131
              | |||||||| || |||| ||| |||||| |||| |||| ||||||||||  | ||||
Db        536 CCAGAGACCCTATTTTTTATGCACATCATGCGAATATCGACAGAATGTGGTCAGTTTGGA 595

Qy       1132 AGACCCTAGGAGGGCCGCGGAGGACGGACTTAACAGATCCAGATTTTCTTGATGCGTCTT 1191
              | || ||||||||     | ||||  || || |||||  ||| |  ||||||   | |
Db        596 AAACTCTAGGAGG---AAGAAGGAATGATTTTACAGATAAAGACTGGCTTGATTTTTTGT 652

Qy       1192 TCGTTTTTTATGACGAAAA 1210
              || | || || |||||  ||
Db        653 TCTTGTTCTACGACGAGAA 671


RESULT 12
US-09-443-067-29
; Sequence 29, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
;  APPLICANT: ORGANISATION
;  TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
;  TITLE OF INVENTION: pineapple
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/443,067
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: US 08/976, 222
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: PCT/AU98/00362
;  EARLIER FILING DATE: 1998-05-19
;  EARLIER APPLICATION NUMBER: AU PP3898
;  EARLIER FILING DATE: 1995-05-23
;  EARLIER APPLICATION NUMBER: AU PP6849
;  EARLIER FILING DATE: 1997-05-19
;  EARLIER APPLICATION NUMBER: AU PP5600
;  EARLIER FILING DATE: 1995-09-26
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
;   LENGTH: 2057
;   TYPE: DNA
;   ORGANISM: lettuce
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)..(1842)
US-09-443-067-29

  Query Match            13.3%;  Score 258.8;  DB 4;  Length 2057;
  Best Local Similarity  53.2%;  Pred. No. 1e-68;
  Matches  754;  Conservative    0;  Mismatches  622;  Indels   42;  Gaps    8;

Qy        388 TACCACCTCCCTCCACTACCATGAGGGTTCGCCGTGCGGCTCATTTAGTTGATGATGCAT 447
              | |  ||| |   | ||   ||  | ||||| |  || || ||   ||    ||  | |
Db        431 TCCTTCCTTCAAACCCTGTGATTCGTGTTCGACCAGCTGCACAGAAAGCCACTGCCGATT 490

Qy        448 ACATTGCCAAATTCAAGAAAGCCGTTGAGCTTATGCGAGCTCTACCTGAGGATGACCCTC 507
              ||| ||| || |   |  ||||  || |   |||   | ||| || |||||  |||| |
Db        491 ACACTGCTAAGTATCAACAAGCAATTCAAGCCATGAAGGATCTCCCCGAGGACCACCCAC 550

Qy        508 GTAGCTTCAAGCAACAAGCTAACGTCCATTGCGCTTACTGCGCGGGGGCGTATAATCAAG 567
              |||||  |||||||||||  ||  | || || |||| |||   || |  || |||||||
Db        551 ATAGCTGGAAGCAACAAGGCAAGATTCACTGTGCTTATTGCAACGGTGGTTACAATCAAG 610

Qy        568 ------CCGGTTTCACAAACCTAAAGCTCCAAATCCACCGATCTTGGCTTTTTTTCCCGT 621
                   |||| | | ||  || | || || || |||   || ||||| || || || | |
Db        611 AACAAAGTGGTTACCCGAATTTACAACTTCAGATTCACAACTCATGGCTCTTCTTTCCTT 670

Qy        622 TCCATAGATATTATATCTACTTTTTTGAAAGAATATTGGGAAAACTAATCAATGATACAA 681
              ||||  | |  ||  |||| || |  || |  |||||||| ||  | || |||||| |||
Db        671 TCCACCGGTGGTACCTCTATTTCTACGAGAAGATATTGGGGAAGTTGATTAATGATCCAA 730

Qy        682 CTTTTGCTCTCCAATTTTGGAACTATGATTCACCTGGTGGAATGACAATCCCATCAATGT 741
              |||| ||||| |  |  |||||||  |||  |||  |||||||    || ||  | ||||
Db        731 CTTTCGCTCTACCTTACTGGAACTGGGATAACCCTACTGGAATGGTTATTCCTGCCATGT 790

Qy        742 TTATTGATACTAA------TTCTTCGCTGTACGATAGTTTACGGGACAGTAATCATCAGC 795
              |     | |  |      |   || |||| ||  |||| ||||    || || |  |
Db        791 TCGAACAGAACAGCAAAACTAACTCTCTGTTTGACCCTTTAAGGGATGCGAAACACCTCC 850

Qy        796 CACCAACCATCGTAGACTTGAACTACGCCTTTTCTGATTCCGACAATACCACTACTCCTG 855
              ||||  | ||| | ||  |  | || |      ||| | | |||| |    | |||  |
Db        851 CACCTTCTATCTTTGATGTTGAATATG------CTGGTGCAGACACTGGTGCCACTTGTA 904

Qy        856 AAGAGCAAATGATTATAAACCTTAAAATTGTGTACAGACAAATGGTGTCGAGCGCTAAGA 915
              ||| || ||    || || ||          |||||||||| |||||  | | | | |
Db        905 TAGACCAGATAGCCATTAATCTGTCTTCAATGTACAGACAGATGGTCACCAACTCCACTG 964

Qy        916 CTCCACAGCTTTTCTTCGGCCGCCCATACCGACGTGGGGACCA------------AGAGT 963
              | || | |  ||||||||  ||  ||    | ||| |  |                ||||
Db        965 ATACAAAACGATTCTTCGGTGGCGAATTTGTAGCTGGAAATGACCCTCTTGCGAGCGAGT 1024

Qy        964 TTCCCGGGGTGGGGTCGATTGAGTTAGTCCCTCATGGCATGATACATTTATGGACCGGTT 1023
              |   ||  | ||| |  | ||     |   |||       |   ||    |||   |||
Db       1025 TCAACGTAGCTGGGACCGTAGAAGCTGGGGTTCACACTGCGGCTCACCGCTGGGTGGGTA 1084

Qy       1024 CTGAGAACACGCCCTATGGCGAGAACATGGGGGCTTTCTACTCAACGGCTAGAGACCCGA 1083
              |   | | | || |  |||| ||||||||   ||||||||  | |     || ||
Db       1085 ATTCTAGGATGGCCAACAGCGAAGACATGGGGAACTTCTACTCCGCAGGATATGATCCTC 1144

Qy       1084 TATTTTTTGCTCATCATTCGAACGTCGATAGAATGTGGTCCATATGGAAGACCCTAGGAG 1143
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Db       1145 TCTTTTACGTCCACCATGCGAATGTCGACAGGATGTGGCAAATCTGGAAAGATATTGACA 1204

Qy       1144 GGCCGCGGAGGACGGACTTAACAGATCCAGATTTTCTTGATGCGTCTTTCGTTTTTTATG 1203

Db       1205 AGAAGACACACAAGGATCCGACCTCTGGCGACTGGCTAAATGCATCATACGTGTTTTACG 1264

Qy       1204 ACGAAAACGCAGAGATGGTTCGGGTCAAGGTTCGGGATTGCTTAGATGAAAAGAAACTAG 1263

Db       1265 ATGAGAATGAAAATCTTGTACGTGTCTACAACCGAGACTGTGTAGACATTAATCGGATGG 1324

Qy       1264 GGTACGTTTATCAAGATGTGGAGATTCCGTGGCTCAACACTCGTCCAACACCAAAAG--- 1320

Db       1325 GATATGACTACGAAAGGTCAGCAATCCCATGGATCCGTAGTCGGCCGACTGCACATGCGA 1384

Qy       1321 TTTCTCCGTCTCTACTTAAGAAATTTCATAGAACAAACACTGCCAATCCGAGACAAGTTT 1380

Db       1385 AGGGGGCGAACGTTGCTGCTAAGTCTGCTGGAATCGTGCAGAAGGTGGAGGATATCGTAT 1444

Qy       1381 TTCCTGCGATACTTGACAGAGTCTTAAAAGTTATCGTGACGAGGCCGAAGAAAACTAGAA 1440

Db       1445 TCCCGCTGAAGTTAAACAAGATAGTGAAGGTTCTAGTGAAGAGGCCAGCTACAAACAGGA 1504

Qy       1441 GTAGGAAAGAAAAGGACGAGTTAGAAGAGATTTTAGTGATTGAAGGGATTGAACTGGAAA 1500

Db       1505 CCAAGGAGGGAAAGGAGAAAGCAAATGAGCTGTTGTTCGTGAATGGAATCACGTTTGATG 1564

Qy       1501 GAGACCACGGGCACGTAAAATTCGACGTTTATATTAATGCTGACGAAGATGACCTTGCGG 1560

Db       1565 CTGAGC---GGTTTCTAAAGATTGACGTGTTTGTCAACGACGTCGACGATGGAATT---C 1618

Qy       1561 TGATTTCGCCGGAGAATGCTGAGTTCGCCGGGAGTTTCGTGAGTCTGTGGCACAAACCTA 1620

Db       1619 AGACCACCGCTGCTGATAGTGAGTTTGCTGGTAGTTTCGCACAGTTGCCACATAACCAT- 1677

Qy       1621 TAAAGGGGAAGAGGACAAAGACGCAGTTATTAACATTGTCGATTTGTGATATTTTGGAGG 1680

Db       1678 --GGCGACAAGATGTTTATGAGGAGTGGGGCAGCGTTCGGGATCACGGAGCTCTTGGAAG 1735

Qy       1681 ATTTGGATGCTGACGAAGATGATTATGTGTTGGTCACTTTGGTTCCGAGAAACGCCGGAG 1740

Db       1736 ACATTGAAGCTGAAGGTGATGACTCTGTTGTTGTGACATTGGTGCCGAGAACAGGGTGTG 1795

Qy       1741 ATGCGATCAAGATTCATAATGTCAAGATTGAGCTTGAT 1778

Db       1796 ATGAAGTAACTATTGGCGAGATCAAGATTCAGCTGGTT 1833
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RESULT 13
US-09-889-463A-25
; Sequence 25, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 988
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (962)
; OTHER INFORMATION: n = a, c, g or t

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (970)..(971)
; OTHER INFORMATION: n = a, c, g or t
US-09-889-463A-25

Query Match 13.2%; Score 257.8; DB 4; Length 988;
Best Local Similarity 62.4%; Pred. No. 1.3e-68;
Matches 442; Conservative 0; Mismatches 253; Indels 13; Gaps 2;

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Qy        274 CCGGCCCTATCGCCGCCCCTGATGTCACCAAATGTGGTCAGCCAGACTTGCCACCTGGCA 333

Db        273 CTGCCCCAATACTTGGTCCAGACCTAACCACATGTGTTCAAGCAGAACTACCCGAAGGTG 332

Qy        334 CAGCCCCAATAAACTGTTGTCCCCCAATCCCCGCTAAAATCATCGATTTCGAGCTACCAC 393

Db        333 TAGAACCCACCAATTGTTGTCCCCCAATTTCCACAAACATCATAGATTTCAAGTTCCCTC 392

Qy        394 CTCCCTCCACTACCATGAGGGTTCGCCGTGCGGCTCATTTAGTTGATGATGCATACATTG 453

Db        393 CCTCCAACCAACCCTTGCGTGTACGATCCGCTGCTCATCTGGTCAACAAAGACTATCTAG 452

Qy        454 CCAAATTCAAGAAAGCCGTTGAGCTTATGCGAGCTCTACCTGAGGATGACCCTCGTAGCT 513

Db        453 CTAAATACGAGAAAGCCGTTAACCTGATGAAAAATCTCCCGTCAGATGATCCACGTAGTT 512

Qy        514 TCAAGCAACAAGCTAACGTCCATTGCGCTTACTGCGCGGGGGCGTATAATCAAGCCGGTT 573

Db        513 TCGCGCAACAAGCCAAAGTTCATTGTGCTTATTGCGACGGTGGATATCACCAACTAGGCT 572

Qy        574 TCACAAACCTAAAGCTCCAAATCCACCGATCTTGGCTTTTTTTCCCGTTCCATAGATATT 633

Db        573 TCCCTGACCTTGATCTCGAAGTGCACTTCTCTTGGCTCTTCTTTCCTTACCACAGATGGT 632

Qy        634 ATATCTACTTTTTTGAAAGAATATTGGGAAAACTAATCAATGATACAACTTTTGCTCTCC 693

Db        633 ATCTCTATTTCCATGAAAGGATATTGGCGAGCTTGATCAATGATCCAACCTTTGCTCTTC 692

Qy        694 AATTTTGGAACTATGATTCACCTGGTGGAATGACAATCCCATCAATGTTTATTGATACTA 753

Db        693 CATTTTGGAACTGGGATGCTCCTGGGGGCATGCAACTTCCTTCCATGTACGCAGATCCCA 752

Qy        754 ATTCTTCGCTGTACGATAGTTTACGGGACAGTAATCATCAGCCACCAACCATCGTAGACT 813

Db        753 AATCACCCCTTTATGATTCTCTACGCAATGCCAACCATCAACCACCAACACTTGTAAACC 812

Qy        814 TGAACTACGCCTTTTCTGATTCCGACAATACCACTACTCCTGAAGAGCAAATGATTATAA 873

Db        813 TTGACTTTACTATCGAGGAT----------CCTAATGCAGAGGCAAATATCTCCACCA 860

Qy        874 ACCTTAAAATTGTGTACAGACAA-ATGGTGTCGAGCGCTAAGACTCCACAGCTTTTCTTC 932

Db        861 ACCTCACCACAATGTATAGGCAAGCTTGTGTCTAACGCAAAGACTCCAACATTGTTCTTC 920

Qy        933 GGCCGCCCATACCGACGTGGGGACCAAGAGTTTCCCGGGGTGGGGTCG 980

Db        921 GGAAATCCTTATCGTGCTGGGGATCAGCTAACCCTGGTGGGNGGTCCG 968
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RESULT 14
US-09-129-030-35
; Sequence 35, Application US/09129030A
; Patent No. 6242221
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
; TITLE OF INVENTION: GENOMIC PPO CLONES
; FILE REFERENCE: 57072-PCT-US
; CURRENT APPLICATION NUMBER: US/09/129,030A
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: AU PN7856
; EARLIER FILING DATE: 1996-02-05
; EARLIER APPLICATION NUMBER: AU PO2361
; EARLIER FILING DATE: 1996-09-16

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;  EARLIER APPLICATION NUMBER: PCT/AU97/00041
;  EARLIER FILING DATE: 1997-01-24
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: FRENCH BEAN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(660)
US-09-129-030-35

  Query Match            12.8%;  Score 249.4;  DB 3;  Length 662;
  Best Local Similarity  62.9%;  Pred. No. 3.8e-66;
  Matches  426;  Conservative    0;  Mismatches  236;  Indels   15;  Gaps    2;

Qy        534 CATTGCGCTTACTGCGCGGGGGCGTATAATCAAGCCGGTTTCACAAACCTAAAGCTCCAA 593
              ||||| || || || |  || || ||| | ||||  || ||| |  ||||  | ||||||
Db          1 CATTGTGCGTATTGTGACGGTGCATATCACCAAGTTGGGTTCCCTGACCTTGATCTCCAA 60

Qy        594 ATCCACCGATCTTGGCTTTTTTTCCCGTTCCATAGATATTATATCTACTTTTTTGAAAGA 653
              |||||   |||||||| || || || |||||| |||  ||| |||| || |  ||||||
Db         61 GTCCACAACTCTTGGCTCTTCTTTCCCTTCCATCGATGGTATCTCTATTTCTACGAAAGA 120

Qy        654 ATATTGGGAAAACTAATCAATGATACAACTTTTGCTCTCCAATTTTGGAACTATGATTCA 713
              || ||||| |   | ||||| ||  |||| || || ||||  |||||||||  ||| |
Db        121 ATCTTGGGGAGCTTGATCAACGACCCAACCTTCGCCCTCCCGTTTTGGAACTGGGATGCT 180

Qy        714 CCTGGTGGAATGACAATCCCATCAATGTTTATTGATACTAATTCTTCGCTGTACGATAGT 773
              ||    || |||  | | || || || | |   ||  |||| ||  | || || |||  |
Db        181 CCCAAGGGCATGCAACTTCCTTCCATTTATGCAGACCCTAAATCACCTCTCTATGATCCT 240

Qy        774 TTACGGGACAGTAATCATCAGCCACCAACCATCGTAGACTTGAACTACGCCTTTTCTGAT 833
              | ||  |   |||||||| || ||||  |||| ||| |  ||| || | ||   |||
Db        241 CTTCGCAATTCTAATCATCAACCTCCAACACTCGTTGACCTTGACTTCGACATTGAGGAT 300

Qy        834 TCCGACAATACCACTACTCCTGAAGAGCAAATGATTATAAACCTTAAAATTGTGTACAGA 893
              | ||             | | || |   ||||       |||||||  ||  |||| ||
Db        301 CCTGA------------TGCCGATGGAAAAATCTCCTCCAACCTTACCATAATGTATAGG 348

Qy        894 CAAATGGTGTCGAGCGCTAAGACTCCACAGCTTTTCTTCGGCCGCCCATACCGACGTGGG 953
              ||| | ||||| |  |  || |||||     || ||| | ||     | |||||   |||
Db        349 CAAGTTGTGTCTAATGGGAAAACTCCTAGACTGTTCCTTGGAAATGCTTACCGTGCTGGA 408

Qy        954 GACCAAGAGTTTCCCGGGGTGGGGTCGATTGAGTTAGTCCCTCATGGCATGATACATTTA 1013
              ||  ||        || || |  || ||  | |||   || || |||||      | ||| ||
Db        409 GATGAACCCGACCCGGGTGGTGGATCCGTAGAGAACGTTCCACATGGACCTGTTCATGTA 468

Qy       1014 TGGACCGGTTCTGAGAACACGCCCTATGGCGAGAACATGGGGGCTTTCTACTCAACGGCT 1073
              |||||||||  |     ||  |||| |     |||||||||||  |||||| ||   | ||
Db        469 TGGACCGGTGATATCGACCAGCCCAACATTGAGAACATGGGAACTTTCTATTCGGCTGCA 528

Qy       1074 AGAGACCCGATATTTTTTGCTCATCATTCGAACGTCGATAGAATGTGGTCCATATGGAAG 1133
              ||||||||  || || ||  |||||||||| ||   | ||||| ||||||||||||||||
Db        529 AGAGACCCCATTTTCTTCTCTCATCATTCCAATATAGATAGGATGTGGTCCATATGGAAA 588

Qy       1134 ACCCTAGGAGGGCCGCGGAGGACGGACTTAACAGATCCAGATTTTCTTGATGCGTCTTTC 1193
              || || || ||   |   || | ||| || |  ||  | ||||   | ||  |      |
Db        589 ACACTTGGTGG---GAAAAGAAGGGATTTCAGTGACTCGGATTGGTTAGAATCTGGGCTT 645

Qy       1194 GTTTTTTATGACGAAAA 1210
              | ||||| ||||| ||
Db        646 CTCTTTTACGACGAGAA 662


RESULT 15
US-09-129-030-11
; Sequence 11, Application US/09129030A
; Patent No. 6242221
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
;  TITLE OF INVENTION: GENOMIC PPO CLONES
;  FILE REFERENCE: 57072-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/129,030A
;  CURRENT FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: AU PN7856
;  EARLIER FILING DATE: 1996-02-05
;  EARLIER APPLICATION NUMBER: AU PO2361
;  EARLIER FILING DATE: 1996-09-16
;  EARLIER APPLICATION NUMBER: PCT/AU97/00041
;  EARLIER FILING DATE: 1997-01-24
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 590
;   TYPE: DNA
;   ORGANISM: AVOCADO
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(588)
US-09-129-030-11

  Query Match            11.9%;  Score 233;  DB 3;  Length 590;
  Best Local Similarity  64.3%;  Pred. No. 4.1e-61;
  Matches  385;  Conservative    0;  Mismatches  205;  Indels    9;  Gaps    2;

Qy        612 TTTTTCCCGTTCCATAGATATTATATCTACTTTTTTGAAAGAATATTGGGAAAACTAATC 671
              ||||| |||||||||| | || ||  |||||||| | ||| |  || ||||| ||  | ||
Db          1 TTTTTGCCGTTCCATCGTTACTACCTCTACTTCTATGAGAAGATCTTGGGCAAGTTGATT 60

Qy        672 AATGATACAACTTTTGCTCTCCAATTTTGGAACTATGATTCACCTGGTGGAATGACAATC 731
                  |||   || ||||||||||  || |||||||  ||| |||| |||||||||| ||||
Db         61 GGAGATGAGACATTTGCTCTCCCCTTCTGGAACTGGGATGCACCGGGTGGAATGCCAATG 120

Qy        732 CCATCAATGTTTATTGATACTAATTCTTCGCTGTACGATAGTTTACGGGACAGTAATCAT 791
              || || ||||      |  |    ||  |||| |||||      |  | |||   || ||
Db        121 CCGTCCATGTACGCCAAACCATCGTCGCCGCTCTACGACGAGCTGAGAGACGCCAAGCAC 180

Qy        792 CAGCCACCAACCATCGTAGACTTGAACTACGCCTTTTCTGATTCCGACAATACCACTACT 851
              ||||| || ||  | || ||  || |||||  |||    ||| ||  ||| |||   |
Db        181 CAGCCGCCGACGCTGGTGGATCTGGACTACAACTTCCAGGATCCCACCAACACCGACA-- 238

Qy        852 CCTGAAGAGCAAATGATTATAAACCTTAAAATTGTGTACAGACAAATGGTGTCGAGCGCT 911
                  |  |||| ||     | |||||     ||  ||||| | ||  |||||||||  |
Db        239 ----AGCAGCAGATAGCCAGCAACCTCTCCATCATGTACCGGCAGGTGGTGTCGAATGGC 294

Qy        912 AAGACTCCACAGCTTTTCTTCGGCCGCCCATACCGACGTGGGGACCAAGAGTTTCCCGGG 971
              |||||  | ||| | ||| | ||     | |||||     || |   |   |  |||||
Db        295 AAGACGGCGCAGTTGTTCATGGGTGCGGCGTACCGGGCCGGCGGGGAGCCGGACCCCGGT 354

Qy        972 GTGGGGTCGATTGAGTTAGTCCCTCATGGCATGATACATTTATGGACCGGTTCTGAGAAC 1031
              |  |||||| | |||    || || |||||    | | ||| | |||||||||      ||
Db        355 GCCGGGTCGCTAGAGAACGTGCCGCATGGGCCGGTCCATATCTGGACCGGTGACCGGACT 414

Qy       1032 ACGCCCTATGGCGAGAACATGGGGGCTTTCTACTCAACGGCTAGAGACCCGATATTTTTT 1091
                |||| |    ||||||||||||   ||||||||  |||| || |||||||| || ||
Db        415 CAGCCCAACACGGAGAACATGGGGAACTTCTACTCGGCGGCAAGGGACCCGATCTTCTTC 474

Qy       1092 GCTCATCATTCGAACGTCGATAGAATGTGGTCCATATGGAAGACCCTAGGAGGGCCGCGG 1151
              || || || ||||||||||  | ||||||  | | ||||||||||| |||||   |  |
Db        475 GCCCACCACTCGAACGTCGACCGGATGTGGAGCGTGTGGAAGACCCTGGGAGG---GAAG 531

Qy       1152 AGGACGGACTTAACAGATCCAGATTTTCTTGATGCGTCTTTCGTTTTTTATGACGAAAA 1210
              |||| |||||| || || |||||||   ||  |  ||  ||| |||| || ||||||||
Db        532 AGGAAGGACTTCACTGACCCAGATTGGCTCAACTCGGGCTTCCTTTTCTACGACGAAAA 590


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GenCore version 5.1.6

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(without alignments)
856.179 Million cell updates/sec

Title: US-09-446-089E-2
Perfect score: 2991
Sequence: 1 MFKNPNIRYHKLSSKSNDND.....VPRNAGDAIKIHNVKIELDG 562

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1560.5	52.2	599	4	US-09-889-463A-20	Sequence 20, Appl
2	1539.5	51.5	599	4	US-09-889-463A-28	Sequence 28, Appl
3	1531.5	51.2	619	4	US-09-443-067-20	Sequence 20, Appl
4	1520.5	50.8	601	4	US-09-889-463A-10	Sequence 10, Appl
5	1477	49.4	607	4	US-08-482-934A-2	Sequence 2, Appli
6	1309	43.8	601	4	US-09-889-463A-36	Sequence 36, Appl
7	1292	43.2	557	4	US-09-889-463A-14	Sequence 14, Appl
8	1254	41.9	619	4	US-09-889-463A-32	Sequence 32, Appl
9	1240.5	41.5	423	4	US-09-443-067-26	Sequence 26, Appl
10	1160.5	38.8	587	3	US-08-481-190-4	Sequence 4, Appli
11	1160.5	38.8	587	5	PCT-US93-00869-4	Sequence 4, Appli
12	1120	37.4	596	3	US-08-481-190-8	Sequence 8, Appli
13	1120	37.4	596	5	PCT-US93-00869-8	Sequence 8, Appli
14	1081.5	36.2	609	4	US-09-443-067-30	Sequence 30, Appl
15	1025.5	34.3	588	3	US-08-481-190-16	Sequence 16, Appl
16	1025.5	34.3	588	5	PCT-US93-00869-16	Sequence 16, Appl
17	1022.5	34.2	583	3	US-08-481-190-19	Sequence 19, Appl
18	1022.5	34.2	583	5	PCT-US93-00869-19	Sequence 19, Appl
19	1014.5	33.9	597	4	US-09-889-463A-34	Sequence 34, Appl
20	1003.5	33.6	351	4	US-09-443-067-18	Sequence 18, Appl
21	974	32.6	590	4	US-09-443-067-22	Sequence 22, Appl
22	861	28.8	438	4	US-08-482-934A-12	Sequence 12, Appl
23	844	28.2	441	4	US-08-482-934A-10	Sequence 10, Appl
24	806.5	27.0	222	4	US-09-443-067-16	Sequence 16, Appl
25	794.5	26.6	220	3	US-09-129-030-36	Sequence 36, Appl
26	782.5	26.2	221	4	US-09-889-463A-16	Sequence 16, Appl
27	773.5	25.9	613	4	US-09-889-463A-40	Sequence 40, Appl
28	766.5	25.6	223	3	US-09-129-030-30	Sequence 30, Appl
29	762	25.5	229	3	US-09-129-030-34	Sequence 34, Appl
30	724.5	24.2	284	4	US-09-443-067-6	Sequence 6, Appli
31	722.5	24.2	284	4	US-09-443-067-8	Sequence 8, Appli
32	713.5	23.9	196	3	US-09-129-030-12	Sequence 12, Appl
33	709	23.7	221	3	US-09-129-030-26	Sequence 26, Appl
34	705	23.6	196	3	US-09-129-030-28	Sequence 28, Appl
35	701	23.4	194	4	US-09-443-067-2	Sequence 2, Appli
36	695	23.2	291	4	US-09-443-067-28	Sequence 28, Appl
37	691	23.1	224	3	US-09-129-030-24	Sequence 24, Appl
38	685.5	22.9	222	3	US-09-129-030-32	Sequence 32, Appl
39	674.5	22.6	196	3	US-09-129-030-2	Sequence 2, Appli
40	674	22.5	223	4	US-09-443-067-12	Sequence 12, Appl
41	672.5	22.5	196	3	US-09-129-030-14	Sequence 14, Appl
42	671	22.4	274	4	US-09-889-463A-26	Sequence 26, Appl
43	658	22.0	227	4	US-09-443-067-14	Sequence 14, Appl
44	623.5	20.8	226	3	US-09-129-030-52	Sequence 52, Appl
45	588	19.7	265	4	US-09-889-463A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-889-463A-20
; Sequence 20, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Glycine max
US-09-889-463A-20

Query Match 52.2%; Score 1560.5; DB 4; Length 599;
Best Local Similarity 55.9%; Pred. No. 1.2e-153;
Matches 310; Conservative 84; Mismatches 134; Indels 27; Gaps 13;

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Qy         17 NDNDQ-ESSHRCKHILLFIITLFLLIVGLYIANSLAYARFASTSTGPIAAPDVTKCGQPD 75
              | | | |  |   |    ::  |  |   : : |:  :| ||:    ||: ||:  || ||
Db         58 NPNSQGEPPHIVGHRRNVLLGLGGLCGAVTLNNNNPFA-FAA----PISPPDLNTCGPPD 112

Qy         76 LPPGTAPINCCPPIPAKIIDFELPPPSTTMRVRRAAHLVDDAYIAKFKKAVELMRALPED 135
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Db        113 LPAGVKPTNCCPP-SSKIIDFKFSPSNQPLRVRPAAHLVNDEYLAKYKKALDLMKKLPSD 171

Qy        136 DPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIYFFERILGKLINDT 195
              |||:| |||||||||| |||:| || :| ||:| ||||||||||:|:||:|||| ||||
Db        172 DPRNFTQQANVHCAYCDGAYHQVGFPDLDLQVHNSWLFFPFHRWYLYFYERILGSLINDP 231

Qy        196 TFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNYAFSDSDNTTTPEE 255
              |||| |||:|:| || :||:: |  | |||:||::||||||:|||::   |
Db        232 TFALPFWNWDAPKGMQLPSIYADPKSPLYDTLRNANHQPPTLVDLDFNLED----PISNG 287

Qy        256 QMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVPHGMIHLWTGSENTPY 315
              ::  || |:|||:||: ||| || | ||| ||:  || ||:| |||| :|||||  | |
Db        288 KISNNLTIMYRQVVSNGKTPTLFLGNPYRAGDEPDPGFGSVENVPHGPVHLWTGDINQPN 347

Qy        316 GENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDFLDASFVFYDENAEM 375
              |||| ||| ||||||::||||:|||||||||||| || | || |:|:::|:|||||  :
Db        348 IENMGTFYSAARDPIFYSHHSNIDRMWSIWKTLGGKRR-DFTDSDWLESAFLFYDENKNL 406
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Qy        376 VRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVS----PSLLKKF-----HRTNTANPR 426
              |||||:| || :|||||||||:|||||::|||: |     :| : |     |  |:  |
Db        407 VRVKVKDSLDTRKLGYVYQDVDIPWLNSKPTPRRSRVQKVALAQNFGVGAAHAAETS--R 464

Qy        427 QV-FPAILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYINADED 485
              | || :|| |:  :| || |:||:|||:| ||:|||||| || :  |||||:|| |||
Db        465 NVKFPLVLDSVVSTMVKRPNKSRSKKEKEEEEEVLVIEGIEFER-NTPVKFDVFIN-DED 522

Qy        486 DLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLLTLSICDILEDLDADEDDYVLVTLVPR 545
              |   | |:| |||||||||: |  :   :     | | : |:||:|:|::|| | ||||||
Db        523 D-KQIRPDNTEFAGSFVSVPHSHMHKNKDIITCLRLGLTDLLEELEAEDDDSVRVTLVPR 581

Qy        546 NAGDAIKIHNVKIEL 560
                  :||  :||||
Db        582 YGKGRVKIRGIKIEL 596


RESULT 2
US-09-889-463A-28
; Sequence 28, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 28
;   LENGTH: 599
;   TYPE: PRT
;   ORGANISM: Glycine max
US-09-889-463A-28

  Query Match            51.5%;  Score 1539.5;  DB 4;  Length 599;
  Best Local Similarity  52.9%;  Pred. No. 1.9e-151;
  Matches  306;  Conservative   87;  Mismatches  146;  Indels   39;  Gaps   14;

Qy          2 FKNPNIRYHKLSSKSNDNDQESS-------HRCKHILLFIITLFLLIVGLYIANSLAYAR 54
              :: |   :|      :|| : ::       || ::||| :  |       |   |:: :|
Db         37 YRKPKRHHHIPRVTCSDNQKPNTSGELVLPHR-RNILLGLGGLCGAAATL---NNIPFAN 92

Qy         55 FASTSTGPIAAPDVTKCGQPDLPPGTAPINCCPPIPAKIIDFELPPPSTTMRVRRAAHLV 114
                |      ||  ||:| | | :|| |   | ||||||    ||||: || :  :||| |||||
Db         93 AA-----PILGPDLTTCVQAELPEGVEPTNCCPPISTNIIDFKFPPSNQPLRVRSAAHLV 147

Qy        115 DDAYIAKFKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFF 174
              :  |:||::||| ||: || |||||| ||| |||||| | |:| || :| |::| |||||
Db        148 NKDYLAKYEKAVNLMKNLPSDDPRSFAQQAKVHCAYCDGGYHQLGFPDLDLEVHFSWLFF 207

Qy        175 PFHRYYIYFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQP 234
              |:||:|:|| |||| |||| |||| |||:|:|||| :|||: |  | ||||||::||||
Db        208 PYHRWYLYFHERILASLINDPTFALPFWNWDAPGGMQLPSMYADPKSPLYDSLRNANHQP 267

Qy        235 PTIVDLNYAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVG 294
              ||:|:|::   | :     |  :  ||  :|||:||:|||| |||| ||| |||  || |
Db        268 PTLVNLDFTIEDPN----AEANISTNLTTMYRQLVSNAKTPTLFFGNPYRAGDQPNPGGG 323

Qy        295 SIELVPHGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRT 354
              |:|  ||| :| |||  | |  |:||  |: |||||: ||||||||||||||||| ||
Db        324 SVESTPHGPVHAWTGDINHPTMEDMGNLYAAARDPIFYCHHSNVDRMWSIWKTLGGKRR- 382

Qy        355 DLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTP------- 407
              ||||||:|:::|:|||||  :|||| :|||| :|||||||||:|||| ::|||
Db        383 DLTDPDWLESAFLFYDENKNLVRVKTKDCLDTRKLGYVYQDVDIPWLKSKPTPLRSRAQK 442

Qy        408 -KVSPSL--LKKFHRTNTANPRQV-FPAILDRVLKVIVTRPKKTRSRKEKDELEEILVIE 463
               :::|    :   |   |:  | | || :|| |:  :| ||||:|||:|||:| |||||:|
Db        443 VELTPLFGGVAAAHAAETS--RNVKFPLVLDSVVSTVVKRPKKSRSKKEKEEKEEILVVE 500

Qy        464 GIELERDHGHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTK--TQLLTL 521
              ||| |   | |||||:|| ||||  :: |:| |||||||||: |     | |     | |
Db        501 GIEFESSTG-VKFDVFIN-DEDD-KLVKPDNTEFAGSFVSVPHSHEHHKNNKKIVTCLRL 557

Qy        522 SICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKIE 559
                : |:||:| |::|| |||||||:     : |  :||:
Db        558 GLTDLLEELGAEDDDSVLVTLVPKYGKGRVNIRGIKID 595


RESULT 3
US-09-443-067-20
; Sequence 20, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
;  APPLICANT: ORGANISATION
;  TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
;  TITLE OF INVENTION: pineapple
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/443,067
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: US 08/976, 222
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: PCT/AU98/00362
;  EARLIER FILING DATE: 1998-05-19
;  EARLIER APPLICATION NUMBER: AU PP3898
;  EARLIER FILING DATE: 1995-05-23
;  EARLIER APPLICATION NUMBER: AU PP6849
;  EARLIER FILING DATE: 1997-05-19
;  EARLIER APPLICATION NUMBER: AU PP5600
;  EARLIER FILING DATE: 1995-09-26
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 619
;   TYPE: PRT
;   ORGANISM: pineapple
US-09-443-067-20

  Query Match            51.2%;  Score 1531.5;  DB 4;  Length 619;
  Best Local Similarity  55.6%;  Pred. No. 1.4e-150;
  Matches  296;  Conservative   81;  Mismatches  132;  Indels   23;  Gaps    9;

Qy         43 GLYIANS-LAYARFASTSTGPIAAPDVTKCGQP-DLPPGTAPINCCPPIPAKIIDFELPP 100
              ||| | : |   | |: :  || |||:: || | |||    |  ||||  : ||||:|||
Db         93 GLYGATTGLGLNRRAAAA--PILAPDLSTCGPPADLPASARPTVCCPPYQSTIIDFKLPP 150

Qy        101 PSTTMRVRRAAHLVDDAYIAKFKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYNQAGF 160
              |  :||| ||||||  |:|||:||||||||||| ||||:| ||| |||||| |||:| ||
Db        151 RSAPLRVRPAAHLVDADYLAKYKKAVELMRALPADDPRNFVQQAKVHCAYCDGAYDQIGF 210

Qy        161 TNLKLQIHRSWLFFPFHRYYIYFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTN 220
              :|::||| ||||||:||:|:|  |||||||| | |||| |||:|:|||| ||:: | :
Db        211 PDLEIQIHNSWLFFPWHRFYLYSNERILGKLIGDDTFALPFWNWDAPGGMQFPSIYTDPS 270

Qy        221 SSLYDSLRDSNHQPPTIVDLNYAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFG 280
              ||||| |||: |||||::||:|  : :| | :||||:  || ::|||::|| |||:|| |
Db        271 SSLYDKLRDAKHQPPTLIDLDY--NGTDPTFSPEEQINHNLAVMYRQVISSGKTPELFMG 328

Qy        281 RPYRRGDQEFPGVGSIELVPHGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDR 340
              || |||  || ||:|  ||| :|:|||  | |  |:||  || | ||:|||||  |:||
Db        329 SAYRAGDQPDPGAGSVEQKPHGPVHVWTGDRNQPNREDMGTLYSAAWDPVFFAHHGNIDR 388

Qy        341 MWSIWKTLGGPRRTDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPW 400
              || :|: |||  | : ||||:|:|||:|||||::|||||:|||:   : | ||||||||
Db        389 MWYVWRNLGGKHR-NFTDPDWLNASFLFYDENAQLVRVKVKDCLEADAMRYTYQDVEIPW 447

Qy        401 LNTRPTPKVSPSLLKKFHRTNTANPR--------QVFPAILDRVLKVIVTRPKKTRSRKE 452
              |  :|||| :   :|    |  | ||          || :||: :   | |||  || ||
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Db        448 LKAKPTPKSALQKIKSKVSTLKATPRGTTTTTAETTFPVVLDKPVSATVARPKARRSGKE 507

Qy        453 KDELEEILVIEGIELERDHGHVKFDVYINADEDDLAVISPENAEPAGSFVSLWHKPIKGK 512

Db        508 KEEEEEVLVVEGIELEKD-VFVKFDVYINSPEHE--GVGPEASEFAGSFVHVPHKHKKAK 564

Qy        513 RTKTQL-----LTLSICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKIE 559

Db        565 KGKEMARMNTRLKLGITDLLEDIGAEDDESVLITLVPRSGKGMVKVGGLRID 616


RESULT 4
US-09-889-463A-10
; Sequence 10, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
;   LENGTH: 601
;   TYPE: PRT
;   ORGANISM: Glycine max
US-09-889-463A-10

  Query Match             50.8%;  Score 1520.5;  DB 4;  Length 601;
  Best Local Similarity   55.5%;  Pred. No. 1.9e-149;
  Matches  289;  Conservative   84;  Mismatches  125;  Indels   23;  Gaps    9;

Qy         48 NSLAYARFASTSTGPIAAPDVTKCGQPDLPPGTAPINCCPPIPAKIIDFELPPPSTTMRV 107

Db         93 NPFAPA-------APISPPDLTTCGPPDLPEGAEPTNCCPPFSSTIIDFKFPPSNKPLRV 145

Qy        108 RRAAHLVDDAYIAKFKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYNQAGFTNLKLQI 167

Db        146 RPAAHLVDKNYLAKYKKAIDLMKKLPANDPRNFMQQANVHCAYCTGSYDQVGFPGLELQV 205

Qy        168 HRSWLFFPFHRYYIYFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSL 227

Db        206 HSSWLFFPYHRWFLYFYERILGSLINDPTFALPFWNWDAPKGMQLPSIYADPKSPLYDPL 265

Qy        228 RDSNHQPPTIVDLNYAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGD 287

Db        266 RNANHQPPTLVDFDF---NLDNPIS-NGRISTNLTIMYRQLVSNGKTPTLFLGNPYRAGD 321

Qy        288 QEFPGVGSIELVPHGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKT 347

Db        322 APDPGGGSVEGVPHGPVHLWTGDINQPNIENMGDFYSAARDPIFYSHHSNVDRMWSIWKT 381

Qy        348 LGGPRRTDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTP 407

Db        382 LGGKRR-DFTDSDWLESGLLFYDENKNLVRVKVKDCLDTRKLGYVYQDVEIPWLKSKPSP 440

Qy        408 ---KVSPSLLKKFHRTNTANPRQV-----FPAILDRVLKVIVTRPKKTRSRKEKDELEEI 459

Db        441 RRSRVQKVALGPHFNTGVARAAETSRNVQFPLVLDSVVSIVVKRPKKSRSKKEKEEEEEV 500

Qy        460 LVIEGIELERDHGHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLL 519

Db        501 LVIEGVEYD-SNIPVKFDVLIN-DEDD-KQIQPEDSEYAGSFVTVPHSHKHKNKKIITCL 557

Qy        520 TLSICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKIEL 560

Db        558 RLGLTDLLEELEAEDDDSVVVTLVPRYGKGRVQIGGIKIDL 598
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RESULT 5
US-08-482-934A-2
; Sequence 2, Application US/08482934A
; Patent No. 6703542
;  GENERAL INFORMATION:
;    APPLICANT:  Robinson, Simon P.
;    APPLICANT:  Dry, Ian B.
;    TITLE OF INVENTION:  Polyphenol Oxidase Genes
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,934A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/182,045
;      FILING DATE:  14-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/AU92/00356
;      FILING DATE:  16-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PK7248
;      FILING DATE:  17-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John P. White
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  51461-Z/JPW/GJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  607 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-482-934A-2

  Query Match             49.4%;  Score 1477;  DB 4;  Length 607;
  Best Local Similarity   50.3%;  Pred. No. 6.6e-145;
  Matches  287;  Conservative  105;  Mismatches  139;  Indels   40;  Gaps   12;

Qy          4 NPNIRYHKLSSKSNDNDQESSHRC--KHILLFIITLFLLIVGLYIANSLAYARFASTSTG 61

Db         58 DPN------SDSTSDVRETSSGKLDRRNVLLGIGGLYGAAGGLGATKPLAFG-------A 104

Qy         62 PIAAPDVTKCGQPDLPPGTAPINCCPPIPAKIIDFELPPPSTTMRVRRAAHLVDDAYIAK 121

Db        105 PIQAPDISKCGTATVPDGVTPTNCCPPVTTKIIDFQLPSSGSPMRTRPAAHLVSKEYLAK 164

Qy        122 FKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYI 181

Db        165 YKKAIELQKALPDDDPRSFKQQANVHCTYCQGAYDQVGYTDLELQVHASWLFLPFHRYYL 224

Qy        182 YFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLN 241

Db        225 YFNERILAKLIDDPTFALPYWAWDNPDGMYMPTIYASSPSSLYDEKRNAKHLPPTVIDLD 284

Qy        242 YAFSDSDNTTTPEEQM-IINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVP 300
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Db        285 Y---DGTEPTIPDDELKTDNLAIMYKQIVSGATTPKLFLGYPYRAGDAIDPGAGTLEHAP 341

Qy        301 HGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPD 360

Db        342 HNIVHKWTGLADKP-SEDMGNFYTAGRDPIFFGHHANVDRMWNIWKTIGGKNRKDFTDTD 400

Qy        361 FLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWL--NTRPTPKVSPSLLKKFH 418

Db        401 WLDATFVFYDENKQLVKVKVSDCVDTSKLRYQYQDIPIPWLPKNTKAKAKTT----TKSS 456

Qy        419 RTNTANPRQV----------FPAILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELE 468

Db        457 KSGVAKAAELPKTTISSIGDFPKALNSVIRVEVPRPKKSRSKKEKEDEEEVLLIKGIELD 516

Qy        469 RDHGHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLLTLSICDILE 528

Db        517 REN-FVKFDVYIN--DEDYSVSRPKNSEFAGSFVNVPHKHMKEMKTKTN-LRFAINELLE 572

Qy        529 DLDADEDDYVLVTLVPRNAGDAIKIHNVKIE 559

Db        573 DLGAEDDESVIVTIVPRAGGDDVTIGGIEIE 603


RESULT 6
US-09-889-463A-36
; Sequence 36, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
;   LENGTH: 601
;   TYPE: PRT
;   ORGANISM: Glycine max
US-09-889-463A-36

  Query Match           43.8%;  Score 1309;  DB 4;  Length 601;
  Best Local Similarity   51.7%;  Pred. No. 2.3e-127;
  Matches  258;  Conservative   81;  Mismatches  146;  Indels   14;  Gaps   11;

Qy         67 DVTKCGQPDLPP-GTAPINCCP--PIPAKIIDF-ELPPPSTTMRVRRAAHLVDDAYIAKF 122

Db        106 NVSKCFPVELPSFAITNSHCCPPRPPPSKIIDFKDFASPNATLRVRKPAHMVDEEYIAKL 165

Qy        123 KKAVELMRALPEDDPRSFKQQANVHCAYCAGAYN-QAGFTNLKLQIHRSWLFFPFHRYYI 181

Db        166 EKGIALMKALPDDDPRNFIQQAKVHCAYCNGAYHLPHPFQNTKLNIHRSWFFFPFHRWYI 225

Qy        182 YFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLN 241

Db        226 YFFERILGSLLGDPNFALPFWNWDAVEGMQMPPYFANPNSSLYHKLRNPKHLPPQVVDLN 285

Qy        242 YAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVPH 301

Db        286 YDPFDFNDDTPSHQQVSYNLAFMYKQMV-LASTKELFMGSPFRLGDNPTPGIGSIEAAPH 344

Qy        302 GMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDF 361

Db        345 NTVHKWVGAADKPHQEDMGTFYTAARDPVFYPHHTNSDRLWGIWKKLGEGRKDYSDDPDW 404

Qy        362 LDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSLLKKFHRTN 421

Db        405 LDSDFYFYDENANFVRVKVRDCFDTKRLGYVYEDVDLPWLRTPPTSRKSKLLREAKKGSL 464

Qy        422 TANPRQVFPAILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYIN 481

Db        465 LSSKPWKFPLVLDSITSIVVKRPKKWRSKEEKEQEEEVLVIEGIEFGSDK-YVKFDVHID 523

Qy        482 ADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLLTLSICDILEDLDADEDDYVLVT 541

Db        524 DDEDNLS--GPDETEFVGSFVNVQHG--HGHNVKTS-FKVGISKVLESVEAEEDDEVLVS 578

Qy        542 LVPR-NAGDAIKIHNVKIE 559

Db        579 LVPKVGKGDAI-IGGIKIE 596


RESULT 7
US-09-889-463A-14
; Sequence 14, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
;   LENGTH: 557
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-09-889-463A-14

  Query Match           43.2%;  Score 1292;  DB 4;  Length 557;
  Best Local Similarity   49.3%;  Pred. No. 1.2e-125;
  Matches  260;  Conservative   80;  Mismatches  161;  Indels   26;  Gaps   10;

Qy         39 LLIVGLYIANSLAYARFASTSTGPIAAPDVTKCGQPDLPPGTAP-INCCPPIPAKIIDFE 97

Db         46 LLGLGSAAAAGLGAQRARGAIAAPIQAPDLGNCNPPDL-PNTAPDTNCCPTSGTGIIDFV 104

Qy         98 LPPPSTT-MRVRRAAHLVDDAYIAKFKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYN 156

Db        105 LPPASSAPLRVRPAAHLADAEYLAKYERAVALMKQLPADDPRSFEQQWRVHCAYCDGAYD 164

Qy        157 QAGFTNLKLQIHRSWLFFPFHRYYIYFFERILGKLINDTTFALQFWNYDSPGGMTIPSMF 216

Db        165 QVGFPDLEIQVHNCWLFFPWHRFYLYFHERILGKLIGDDTFALPFWNWDAPDGMTLPAIY 224

Qy        217 IDTNSSLYDSLRDSNHQPPTIVDLNYAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQ 276

Db        225 ANRSSPLYNERRNPAHQPPFPVDLD--FNEIDVIIPTDEQIDQNLNIMYRQMVSGAKKTR 282

Qy        277 LFFGRPYRRGDQEFPGVGSIELVPHGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHS 336

Db        283 LFMGQPYRAGDQPDPGAGSVENVPHGTMHTWTGDPAQPNNEDMGNFYSAARDPIFFAHHG 342

Qy        337 NVDRMWSIWKTLGGPRRTDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDV 396

Db        343 NIDRLWHVWRGL-RPGNADFTDTDWLDTAFLFYDEEARPVRVRVRDCLDPAAMGYAYQDV 401

Qy        397 EIPWLNTRPTPKVSPSLLKKFHRTNTANPRQVFPAILDRVLKVIVTRPKKTRSRKEKDEL 456

Db        402 GLPWLKAKPA---------KRSRRTPAPAAGALPATLRETVRVTVTRPQVSRSDKEKEEA 452

Qy        457 EEILVIEGIELERDHGHVKFDVYINADED--DLAVISPENAEFAGSFVSLWHKPIKGKRT 514

Db        453 EEVLIVEGIQVADHFKFVKFDVLVNAPESGGDAA-----SGYCAGS-VAMTPHMVRTNKK 506
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```
Qy        515 KTQLLTLS---ICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKI 558
              |  : |::   :||::::: || |  |:|:|||| |: : |  | |
Db        507 KGSVKTVARFGVCDLMDNIGADGDKTVVVSLVPRCGGELVTIGGVSI 553


RESULT 8
US-09-889-463A-32
; Sequence 32, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
;   LENGTH: 619
;   TYPE: PRT
;   ORGANISM: Glycine max
US-09-889-463A-32

  Query Match             41.9%;  Score 1254;  DB 4;  Length 619;
  Best Local Similarity   46.5%;  Pred. No. 1.3e-121;
  Matches  270;  Conservative   87;  Mismatches  178;  Indels   46;  Gaps   17;

Qy         11 KLSSKSNDN--------DQESSHRC--KHILLFIITLFLLIVGLYIANSLAYARFASTST 60
              |:|  || |         :: ||:    ||       : | | ||| |::|:     : :
Db         52 KVSCNSNQNTPTPNPEEEKPSSYNILGKHRR----DILLGIGGLYGASALSNTNPLAMAA 107

Qy         61 GPIAAPDVTKCG-QPDLPPG--TAPINCCPP-IPAKIIDFELPPPSTTMRVRRAAHLVDD 116
               ||  ||:  |    |:| |     : ||||   :  |||:| |  | :|||  |  | |
Db        108 APILEPDLEHCCITDDVPKGEIEKQVYCCPPKSSSPPIDFKL-PKGTPLRVRPPAQFVTD 166

Qy        117 AYIAKFKKAVELMRALPEDDPRSFKQQANVHCAYCAGAYNQAGF-TNLKLQIHRSWLFFP 175
              |: |:| |:: || || ||||||||||::||||| | | | ||    |  ::| ||:|||
Db        167 EYLEKYKLALKRMRELPSDDPRSFKQQADIHCAYCDGGYKQLGFPVELDFKVHFSWIFFP 226

Qy        176 FHRYYIYFFERILGKLINDTTFALQFWNYDSP-GGMTIPSMFIDTNSSLYDSLRDSNHQP 234
              |||:|:||:|||| ||:| |||| :||:|:| ||| :||:| | :| |||  |: :  |
Db        227 FHRWYLYFYERILGSLIDDPTFALPYWNWDNPDGGMVLPSIFADEDSPLYDPRRNPDITP 286

Qy        235 PTIVDLNYAFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVG 294
              |:|||||        :  |  :  || ::|  :|| ||   || |:|:  | |      |
Db        287 TTLVDLNYG-------SGKEPSVEQNLGVMYTSVVSGAKRASLFHGKPFLAGKQPELSGG 339

Qy        295 SIELVPHGMIHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRT 354
              ::|| ||  :| |||     |  |:|| |||  ||| |::||:||||||:||||:   :|
Db        340 TVELGPHTAVHRWTGDPRQPNKEDMGRFYSAGRDPAFYSHHANVDRMWNIWKTIPSGKRR 399

Qy        355 DLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSLL 414
              |  : |:|: || |||||  :|||||:| ||  |:|||||| ||||  :| || :
Db        400 DFKNRDWLETSFFFYDENKTLVRVKVKDSLDTNKMGYVYQDVAIPWLEKKPKPKRTRKAK 459

Qy        415 K-----KFHRTNTA-----NPRQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIE 463
              |     :|     |     |   ||  :||  : ::| |||: ||:::|:| ||:|||:
Db        460 KVAFAQQFGGIGAAMAAETGPSSKFPLTLLDSKVTLLVKRPKQLRSKRDKEEEEEVLVID 519

Qy        464 GIELERDHGHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIK---GKRTKTQLLT 520
              ||| : |   |||||||   ::|:  | ||: |||||| :| |         |: ||  || .
Db        520 GIEFDGD-DDVKFDVYIT--DEDVEDIGPESTEFAGSFSTLGHSHSNMNMDKKIKTS-LT 575

Qy        521 LSICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKIELD 561
              | | |:||||||: || ||||||||:    | | |:||| :
Db        576 LGITDLLEDLDAENDDSVLVTLVPRSENVTITIQNIKIEFE 616


RESULT 9
US-09-443-067-26
; Sequence 26, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
;  APPLICANT: ORGANISATION
;  TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
;  TITLE OF INVENTION: pineapple
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/443,067
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: US 08/976, 222
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: PCT/AU98/00362
;  EARLIER FILING DATE: 1998-05-19
;  EARLIER APPLICATION NUMBER: AU PP3898
;  EARLIER FILING DATE: 1995-05-23
;  EARLIER APPLICATION NUMBER: AU PP6849
;  EARLIER FILING DATE: 1997-05-19
;  EARLIER APPLICATION NUMBER: AU PP5600
;  EARLIER FILING DATE: 1995-09-26
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: pineapple
US-09-443-067-26

  Query Match             41.5%;  Score 1240.5;  DB 4;  Length 423;
  Best Local Similarity   54.7%;  Pred. No. 1.8e-120;
  Matches  233;  Conservative   70;  Mismatches  104;  Indels   19;  Gaps    6;

Qy        147 HCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIYFFERILGKLINDTTFALQFWNYDS 206
              ||||| |||:| || :|::||| |||||||:||:|:|  |||||||| | |||| |||:|:
Db          1 HCAYCDGAYDQIGFPDLEIQIHNSWLFFPWHRFYLYSNERILGKLIGDDTFALPFWNWDA 60

Qy        207 PGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNYAFSDSDNTTTPEEQMIINLKIVYR 266
              ||||  ||:: | :||||| |||: |||||::||:|  : :| | :||||:  || ::||
Db         61 PGGMQFPSIYTDPSSSLYDKLRDAKHQPPTLIDLDY--NGTDPTFSPEEQINHNLAVMYR 118

Qy        267 QMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVPHGMIHLWTGSENTPYGENMGAFYSTA 326
              |::|| |||:|| |  || |||  || ||:|  ||| :|:|||  | |  |:||  || |
Db        119 QVISSGKTPELFMGSAYRAGDQPDPGAGSVEQKPHGPVHVWTGDRNQPNREDMGTLYSAA 178

Qy        327 RDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDFLDASFVFYDENAEMVRVKVRDCLDE 386
              ||:||||| |:|||| :|: |||  | : ||||:|:|||:||||||::|||||:|||:
Db        179 WDPVFFAHHGNIDRMWYVWRNLGGKHR-NFTDPDWLNASFLFYDENAQLVRVKVKDCLEA 237

Qy        387 KKLGYVYQDVEIPWLNTRPTPKVSPSLLKKFHRTNTANPR--------QVFPAILDRVLK 438
              :  | |||||||||  :|||| :   :|    |  | ||          || :||: :
Db        238 DAMRYTYQDVEIPWLKAKPTPKSALQKIKSKVSTLKATPRGTTTTTAETTFPVVLDKPVS 297

Qy        439 VIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYINADEDDLAVISPENAEFA 498
              | |||  || |||:| ||:||:|||||||:|   |||||||: | :   : || :|||
Db        298 ATVARPKARRSGKEKEEEEEVLVVEGIELEKD-VFVKFDVYINSPEHE--GVGPEASEFA 354

Qy        499 GSFVSLWHKPIKGKRTKTQL-----LTLSICDILEDLDADEDDYVLVTLVPRNAGDAIKI 553
              |||| : ||  | |: }        | | | |:|||: |::|: ||:|||||:    :|:
Db        355 GSFVHVPHKHKKAKKGKEMARMNTRLKLGITDLLEDIGAEDDESVLITLVPRSGKGMVKV 414

Qy        554 HNVKIE 559
                ::|:
Db        415 GGLRID 420


RESULT 10
US-08-481-190-4
; Sequence 4, Application US/08481190
; Patent No. 6160204
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
```

```
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNA
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticutt
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,190
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  203,533
;      FILING DATE:  02-24-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  UA 816 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  587 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-481-190-4

  Query Match             38.8%;  Score 1160.5;  DB 3;  Length 587;
  Best Local Similarity   44.0%;  Pred. No. 7e-112;
  Matches  249;  Conservative   94;  Mismatches  180;  Indels   43;  Gaps   17;

Qy         11 KLSSKSNDNDQESSHRCKHILLFIITLFLLIVGLYIANSLAYARFASTSTGPIAAPDVTK 70
              |:|  :|: |:       :  :|      | : ||| | :||       :  ||  ||:
Db         48 KVSCNANNVDKNPDAVDRRNVL------LGLGGLYGAANLA----PLATAAPIPPPDLKS 97

Qy         71 CGQPDLPPGTAPI-NCCPPIPAKI--IDFELPPPSTTMRVRRAAHLVDDAYIAKFKKAVE 127
              ||   :  |   | :||||:| :|  : :   |  | :|:|  ||  |: |:||:: |
Db         98 CGTAHVKEGVDVIYSCCPPVPDEIDSVPYYKFPSMTKLRIRPPAHAADEEYVAKYQLATS 157

Qy        128 LMRALPED--DPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIYFFE 185
               || | :|  ||  ||||||:||||| |||    |    :||:| ||||||||:|:||:|
Db        158 RMRELDKDPFDPLGFKQQANIHCAYCNGAYKVGG---KELQVHFSWLFFPFHRWYLYFYE 214

Qy        186 RILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNYAFS 245
              |||| |||| |||| :||:| | || || ||    |||||  |: ||:  ||:|| :
Db        215 RILGSLINDPTFALPYWNWDHPKGMRIPPMFDREGSSLYDEKRNQNHRNGTIIDLGHFGK 274

Qy        246 DSDNTTTPEEQ-MIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVPHGMI 304
              : |   ||: | |  || ::|||||::|  |  |||  |  | :  || |:|| :||  :
Db        275 EVD---TPQLQIMTNNLTLMYRQMVTNAPCPSQFFGAAYPLGSEPSPGQGTIENIPHTPV 331

Qy        305 HLWTGSE-NTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDFLD 363
              |:||| :     ||:|| |||   ||||: ||:||||||: || :|| || |||| |:|:
Db        332 HIWTGDKPRQKNGEDMGNFYSPGLDPIFYCHHANVDRMWNEWKLIGGKRR-DLTDKDWLN 390

Qy        364 ASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSLLKKFHRTNTA 423
              : | |||||    |||  |||| ||:|: |  :  || | :|  | |     | :  : |
Db        391 SEFFFYDENRNPYRVKSVDCLDSKKMGFDYAPMPTPWRNFKPIRKSSSG---KVNTASIA 447

Qy        424 NPRQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYINA 482
                :||| | ||| :   :|||  :|: :||:| ||||    |  : |  :|:|||::|
Db        448 PVSKVFPLAKLDRAISFSITRPASSRTTQEKNEQEEILTFNKISYD-DRNYVRFDVFLNV 506

Qy        483 DE----DDLAVISPENAEFAGSFVSLWHKPIKGKRTK---TQLLTLSICDILEDLDADED 535
              |:    |:|     : ||||||: || |  : |  |    :    |:| ::|||:  :::
Db        507 DKTVNADEL-----DKAEFAGSYTSLPH--VHGSNTNHVTSVTFKLAITELLEDIGLEDE 559

Qy        536 DYVLVTLVPRNAGDAIKIHNVKIELD 561
              | : |||||:  |: : | :|:|:|:
Db        560 DTIAVTLVPKAGGEEVSIESVEIKLE 585


RESULT 11
PCT-US93-00869-4
; Sequence 4, Application PC/TUS9300869
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNAs: Cloning
;    TITLE OF INVENTION:  and Applications
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00869
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  CRF D-1057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  587 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-00869-4

  Query Match             38.8%;  Score 1160.5;  DB 5;  Length 587;
  Best Local Similarity   44.0%;  Pred. No. 7e-112;
  Matches  249;  Conservative   94;  Mismatches  180;  Indels   43;  Gaps   17;

Qy         11 KLSSKSNDNDQESSHRCKHILLFIITLFLLIVGLYIANSLAYARFASTSTGPIAAPDVTK 70
              |:|  :|: |:       :  :|      | : ||| | :||       :  ||  ||:
Db         48 KVSCNANNVDKNPDAVDRRNVL------LGLGGLYGAANLA----PLATAAPIPPPDLKS 97

Qy         71 CGQPDLPPGTAPI-NCCPPIPAKI--IDFELPPPSTTMRVRRAAHLVDDAYIAKFKKAVE 127
              ||   :  |   | :||||:| :|  : :   |  | :|:|  ||  |: |:||:: |
Db         98 CGTAHVKEGVDVIYSCCPPVPDEIDSVPYYKFPSMTKLRIRPPAHAADEEYVAKYQLATS 157

Qy        128 LMRALPED--DPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIYFFE 185
               || | :|  ||  ||||||:||||| |||    |    :||:| ||||||||:|:||:|
Db        158 RMRELDKDPFDPLGFKQQANIHCAYCNGAYKVGG---KELQVHFSWLFFPFHRWYLYFYE 214

Qy        186 RILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNYAFS 245
              |||| |||| |||| :||:| | || || ||    |||||  |: ||:  ||:|| :
Db        215 RILGSLINDPTFALPYWNWDHPKGMRIPPMFDREGSSLYDEKRNQNHRNGTIIDLGHFGK 274

Qy        246 DSDNTTTPEEQ-MIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQEFPGVGSIELVPHGMI 304
              : |   ||: | |  || ::|||||::|  |  |||  |  | :  || |:|| :||  :
Db        275 EVD---TPQLQIMTNNLTLMYRQMVTNAPCPSQFFGAAYPLGSEPSPGQGTIENIPHTPV 331
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Qy        305 HLWTGSE-NTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDFLD 363
              |:||| :     ||:|| |||   ||||: ||:||||||: || :|| || |||| |:|:
Db        332 HIWTGDKPRQKNGEDMGNFYSPGLDPIFYCHHANVDRMWNEWKLIGGKRR-DLTDKDWLN 390

Qy        364 ASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSLLKKFHRTNTA 423
              : | |||||    |||  |||| ||:|: |  :  || | :|  | |     | :  : |
Db        391 SEFFFYDENRNPYRVKSVDCLDSKKMGFDYAPMPTPWRNFKPIRKSSSG---KVNTASIA 447

Qy        424 NPRQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYINA 482
                :||| | ||| :   :|||  :|: :||:| ||||     |  : |  :|:|||:|
Db        448 PVSKVFPLAKLDRAISFSITRPASSRTTQEKNEQEEILTFNKISYD-DRNYVRFDVFLNV 506

Qy        483 DE----DDLAVISPENAEFAGSFVSLWHKPIKGKRTK---TQLLTLSICDILEDLDADED 535
              |:    |:|     : |||||: || |  : |  |     :    |:| ::|||:  :::
Db        507 DKTVNADEL-----DKAEFAGSYTSLPH--VHGSNTNHVTSVTFKLAITELLEDIGLEDE 559

Qy        536 DYVLVTLVPRNAGDAIKIHNVKIELD 561
              | : |||||:  |: : | :|:|:|:
Db        560 DTIAVTLVPKAGGEEVSIESVEIKLE 585


RESULT 12
US-08-481-190-8
; Sequence 8, Application US/08481190
; Patent No. 6160204
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNA
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticutt
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,190
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  203,533
;      FILING DATE:  02-24-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  UA 816 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  596 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-481-190-8

  Query Match             37.4%;  Score 1120;  DB 3;  Length 596;
  Best Local Similarity   42.0%;  Pred. No. 1.2e-107;
  Matches  240;  Conservative  108;  Mismatches  177;  Indels   46;  Gaps   20;

Qy         11 KLSSKSNDNDQESSHRCKHILLFIITLFLLIVGLY-IANSLAYARFASTSTGPIAAPDVT 69
              |: : : : |: :|   :::||        : ||| :||::  |     |  || :||:
Db         48 KVINNNGNQDETNSVDRRNVLLG-------LGGLYGVANAIPLA----ASATPIPSPDLK 96

Qy         70 KCGQPDLPPG-TAPINCC-PPIPAKI--IDFELPPPSTTMRVRRAAHLVDDAYIAKFKKA 125
                ||:  :  |   | :|| ||:|     | :   |  | :|:|  || ||: ||||:  |
Db         97 TCGRATISDGPLVPYSCCPPPMPTNFDTIPYYKFPSMTKLRIRTPAHAVDEEYIAKYNLA 156

Qy        126 VELMRALPEDDPRS---FKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIY 182
              :  || | : :| :   ||||||:|||| |||   |    :||:| |||||||||:| |
Db        157 ISRMRDLDKTEPLNPLGFKQQANIHCAYCNGAYIIGG---KELQVHNSWLFFPFHRWYFY 213

Qy        183 FFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNY 242
              |:|||||||:| |||| :||:| | || :| ||    ||||  |:   :  |::||
Db        214 FYERILGKLIDDPTFALPYWNWDHPKGMRLPPMFDREGSSLYDERRNQQVRNGTVLDLG- 272

Qy        243 AFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQ-EFPGVGSIELVPH 301
              :| |    ||  : |  || ::|||||::|  | |||| ||  |:  | |  |:|| :||
Db        273 SFGDKVE-TTQLQLMSNNLTLMYRQMVTNAPCPLLFFGAPYVLGNNVEAP--GTIETIPH 329

Qy        302 GMIHLWTG--------SENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRR 353
                :|:| |        : :  |||:|| |||   ||:|: || ||||||: || :|| ||
Db        330 IPVHIWAGTVRGSKFPNGDVSYGEDMGNFYSAGLDPVFYCHHGNVDRMWNEWKAIGGKRR 389

Qy        354 TDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSL 413
              |::: |:|:: | ||||:    |||||||| ||:|| |  :  || | :|  | |
Db        390 -DISEKDWLNSEFFFYDEHKNPYRVKVRDCLDTKKMGYDYAPMPTPWRNFKPKSKASVGK 448

Qy        414 LKKFHRTNTANP-RQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDH 471
              :     |:|  |  :||| | :|: :   :  ||  :|:::||:| ||:|    | : :
Db        449 V----NTSTLPPANEVFPLAKMDKTISFAINRPASSRTQQEKNEQEEMLTFNNIRYD-NR 503

Qy        472 GHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLLT--LSICDILED 529
              |:::|||::| | :::     : ||||||: || |    |:      :   |:| ::|||
Db        504 GYIRFDVFLNVD-NNVNANELDKAEFAGSYTSLPHVHRAGENDHIAKVNFQLAITELLED 562

Qy        530 LDADEDDYVLVTLVPRNAGDAIKIHNVKIEL 560
              :  :::| : |||||:  |: | | ||:|:|
Db        563 IGLEDEDTIAVTLVPKKGGEGISIENVEIKL 593


RESULT 13
PCT-US93-00869-8
; Sequence 8, Application PC/TUS9300869
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNAs: Cloning
;    TITLE OF INVENTION:  and Applications
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00869
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  CRF D-1057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  596 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  peptide
PCT-US93-00869-8

  Query Match             37.4%;  Score 1120;  DB 5;  Length 596;
  Best Local Similarity   42.0%;  Pred. No. 1.2e-107;
  Matches  240;  Conservative  108;  Mismatches  177;  Indels   46;  Gaps   20;

Qy         11 KLSSKSNDNDQESSHRCKHILLFIITLFLLIVGLY-IANSLAYARFASTSTGPIAAPDVT 69
              |: : : : |: :|   :::||        : ||| :||::  |     |  || :||:
Db         48 KVINNNGNQDETNSVDRRNVLLG-------LGGLYGVANAIPLA----ASATPIPSPDLK 96

Qy         70 KCGQPDLPPG-TAPINCC-PPIPAKI--IDFELPPPSTTMRVRRAAHLVDDAYIAKFKKA 125
               ||:  :  |   | :|| ||:|    | :   |  | :|:|  || ||: ||||:  |
Db         97 TCGRATISDGPLVPYSCCPPPMPTNFDTIPYYKFPSMTKLRIRTPAHAVDEEYIAKYNLA 156

Qy        126 VELMRALPEDDPRS---FKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYYIY 182
              :  || | : :| :   ||||||:||||| |||   |    :||:| |||||||||:| |
Db        157 ISRMRDLDKTEPLNPLGFKQQANIHCAYCNGAYIIGG---KELQVHNSWLFFPFHRWYFY 213

Qy        183 FFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDLNY 242
              |:|||||||:| |||| :||:| | || :| ||    |||||  |:    :  |::||
Db        214 FYERILGKLIDDPTFALPYWNWDHPKGMRLPPMFDREGSSLYDERRNQQVRNGTVLDLG- 272

Qy        243 AFSDSDNTTTPEEQMIINLKIVYRQMVSSAKTPQLFFGRPYRRGDQ-EFPGVGSIELVPH 301
              :| |   ||  : |  || ::|||||::|  | |||| ||  |:  | |  |:|| :||
Db        273 SFGDKVE-TTQLQLMSNNLTLMYRQMVTNAPCPLLFFGAPYVLGNNVEAP--GTIETIPH 329

Qy        302 GMIHLWTG--------SENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRR 353
                :|:| |        : :  |||:|| |||   ||:|: || ||||||: || :|| ||
Db        330 IPVHIWAGTVRGSKFPNGDVSYGEDMGNFYSAGLDPVFYCHHGNVDRMWNEWKAIGGKRR 389

Qy        354 TDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKVSPSL 413
               |::: |:|:: | ||||:    |||||||||| ||:|| |  :  || | :|  | |
Db        390 -DISEKDWLNSEFFFYDEHKNPYRVKVRDCLDTKKMGYDYAPMPTPWRNFKPKSKASVGK 448

Qy        414 LKKFHRTNTANP-RQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDH 471
              :      |:|  |  :||| | :|: :   :  ||  :|:::||:| ||:|    | : :
Db        449 V----NTSTLPPANEVFPLAKMDKTISFAINRPASSRTQQEKNEQEEMLTFNNIRYD-NR 503

Qy        472 GHVKFDVYINADEDDLAVISPENAEFAGSFVSLWHKPIKGKRTKTQLLT--LSICDILED 529
              |:::|||::| | :::     : ||||||: || |    |:      :   |:| ::|||
Db        504 GYIRFDVFLNVD-NNVNANELDKAEFAGSYTSLPHVHRAGENDHIAKVNFQLAITELLED 562

Qy        530 LDADEDDYVLVTLVPRNAGDAIKIHNVKIEL 560
              :  :::| : |||||:  |: | | ||:|:|
Db        563 IGLEDEDTIAVTLVPKKGGEGISIENVEIKL 593


RESULT 14
US-09-443-067-30
; Sequence 30, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
;  APPLICANT: ORGANISATION
;  TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
;  TITLE OF INVENTION: pineapple
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/443,067
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: US 08/976, 222
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: PCT/AU98/00362
;  EARLIER FILING DATE: 1998-05-19
;  EARLIER APPLICATION NUMBER: AU PP3898
;  EARLIER FILING DATE: 1995-05-23
;  EARLIER APPLICATION NUMBER: AU PP6849
;  EARLIER FILING DATE: 1997-05-19
;  EARLIER APPLICATION NUMBER: AU PP5600
;  EARLIER FILING DATE: 1995-09-26
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 609
;   TYPE: PRT
;   ORGANISM: lettuce
US-09-443-067-30

  Query Match             36.2%;  Score 1081.5;  DB 4;  Length 609;
  Best Local Similarity   42.4%;  Pred. No. 1.3e-103;
  Matches  234;  Conservative   95;  Mismatches  176;  Indels   47;  Gaps   16;

Qy         37 LFLLIVGLYIANSLAYARFASTSTGPIAAPD-VTKC--------GQPDLPPGTAPINCCP 87
              | | : ||| | :|       |    |||||| :: |           |   | |   |||
Db         73 LLLGLGGLYGAANL--TTIPSAFGIPIAAPDNISDCVAATSNLRNSKDAIRGLA---CCP 127

Qy         88 PIPA--KIIDFELPPPSTTMRVRRAAHLVDDAYIAKFKKAVELMRALPEDDPRSFKQQAN 145
              |: :  | :|: | | :  :||| ||       | ||:::|:: |: |||| | |:|||
Db        128 PVLSTNKPMDYVL-PSNPVIRVRPAAQKATADYTAKYQQAIQAMKDLPEDHPHSWKQQGK 186

Qy        146 VHCAYCAGAYN--QAGFTNLKLQIHRSWLFFPFHRYYIYFFERILGKLINDTTFALQFWN 203
              :||||| | ||  |:|: ||:|||| |||||||||:|:|:|:|||||||| |||| :||
Db        187 IHCAYCNGGYNQEQSGYPNLQLQIHNSWLFFPFHRWYLYFYEKILGKLINDPTFALPYWN 246

Qy        204 YDSPGGMTIPSMFIDTNS---SLYDSLRDSNHQPPTIVDLNYAFSDSDNTTTPEEQMIIN 260
              :|:| || ||:|| : ||    ||:| |||: | ||:|  |: || :|:  |    :|: ||
Db        247 WDNPTGMVIPAMF-EQNSKTNSLFDPLRDAKHLPPSIFDVEYAGADTGATCI--DQIAIN 303

Qy        261 LKIVYRQMVSSAKTPQLFFGRPYRRGD----QEFPGVGSIELVPHGMIHLWTGSENTPYG 316
              |  :|||||:::    : |||  :  |:      ||   |::|   |   | | |:
Db        304 LSSMYRQMVTNSTDTKRFFGGEFVAGNDPLASEFNVAGTVEAGVHTAAHRWVGNSRMANS 363

Qy        317 ENMGAFYSTARDPIFFAHHSNVDRMWSIWKTLGGPRRTDLTDPDFLDASFVFYDENAEMV 376
              |:|| |||   ||:|: ||:|||||| ||| :       | |  |:|:||:||||||  :|
Db        364 EDMGNFYSAGYDPLFYVHHANVDRMWQIWKDIDKKTHKDPTSGDWLNASYVFYDENENLV 423

Qy        377 RVKVRDCLDEKKLGYVYQDVEIPWLNTRPTPKV--------SPSLLKKFHRTNTANPRQV 428
              ||  |||:|  ::|| |:   |||: :|||            |  :::|           |
Db        424 RVYNRDCVDINRMGYDYERSAIPWIRSRPTAHAKGANVAAKSAGIVQKVEDI-------V 476

Qy        429 FPAILDRVLKVIVTRPKKTRSRKEKDELEEILVIEGIELERDHGHVKFDVYINADEDDLA 488
              ||  |::::||:| ||   |::: |::  |:| : ||  : :   :| ||::| | ||
Db        477 FPLKLNKIVKVLVKRPATNRTKEGKEKANELLFVNGITFDAER-FLKIDVFVN-DVDDGI 534

Qy        489 VISPENAEFAGSFVSLWHKPIKGKRTKTQLLTLSICDILEDLDADEDDYVLVTLVPRNAG 548
              :  ::|||||  | |   |      | ::|||::|: || |:|||||
Db        535 QTTAADSEFAGSFAQLPHNH-GDKMFMRSGAAFGITELLEDIEAEGDDSVVVTLVPRTGC 593

Qy        549 DAIKIHNVKIEL 560
              | : |  :||:|
Db        594 DEVTIGEIKIQL 605


RESULT 15
US-08-481-190-16
; Sequence 16, Application US/08481190
; Patent No. 6160204
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNA
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticutt
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,190
;      FILING DATE:
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  203,533
;      FILING DATE:  02-24-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  UA 816 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  588 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-481-190-16

  Query Match            34.3%;  Score 1025.5;  DB 3;  Length 588;
  Best Local Similarity  40.4%;  Pred. No. 8.8e-98;
  Matches  236;  Conservative   93;  Mismatches  180;  Indels   75;  Gaps   21;

Qy         11 KLSSKSNDNDQESSHRC-----KHILLFIITLFLLIVGLYIANSLAYARFASTSTGPIAA 65
              |:|  :|:|  |          :::||        : ||| | :||       |  ||
Db         45 KVSYNANNNVGEHDKNLDTVDRRNVLLG-------LGGLYGAANLA----PLASASPIPP 93

Qy         66 PDVTKCGQPDLPPGT-APINCCPPIPAKI--IDFELPPPSTTMRVRRAAHLVDDAYIAKF 122
              ||:  ||   :  |     :| ||:|  |  : :   || | :|:|  ||  |: |:||:
Db         94 PDLKSCGVAHVTEGVDVTYSCYPPVPDDIDSVPYYKFPPMTKLRIRPPAHAADEEYVAKY 153

Qy        123 KKAVELMRALPED--DPRSFKQQANVHCAYCAGAYNQAGFTNLKLQIHRSWLFFPFHRYY 180
              : |   || | :|  ||  ||||||:||||| |||   |    :||:| ||||||||:|
Db        154 QLATSRMRELDKDSFDPLGFKQQANIHCAYCNGAYKVGG---KELQVHFSWLFFPFHRWY 210

Qy        181 IYFFERILGKLINDTTFALQFWNYDSPGGMTIPSMFIDTNSSLYDSLRDSNHQPPTIVDL 240
              :||:||||| |||| |||| :||:| | || || ||    |||||  |: ||:  ||:||
Db        211 LYFYERILGSLINDPTFALPYWNWDHPKGMRIPPMFDREGSSLYDDKRNQNHRNGTIIDL 270

Qy        241 NYAFSDSDNTTTPEEQ-MIINLKIVYRQMVSSAKTPQLFFGRPYRRG---DQEFPGVGSI 296
               :   : |   ||: | |  || ::|||||::|  |  |||  |  |    ||:  : :
Db        271 GHFGQEVD---TPQLQIMTNNLTLMYRQMVTNAPCPSQFFGAAYLWGLNQVQEWVLLRT- 326

Qy        297 ELVPHGM-----------IHLWTGSENTPYGENMGAFYSTARDPIFFAHHSNVDRMWSIW 345
              |:|  :           :  | |                ||||: ||:||||||  |
Db        327 SLIPRAISGLVIVLDKKTVKTWVIS-----------IQHGLDPIFYCHHANVDRMWDEW 374

Qy        346 KTLGGPRRTDLTDPDFLDASFVFYDENAEMVRVKVRDCLDEKKLGYVYQDVEIPWLNTRP 405
              | :|| || ||:: |:|:: | |||||    ||||||||| ||:|: |  :  || | :|
Db        375 KLIGGKRR-DLSNKDWLNSEFFFYDENRNPYRVKVRDCLDSKKMGFSYAPMPTPWRNFKP 433

Qy        406 TPKVSPSLLKKFHRTNTANPRQVFP-AILDRVLKVIVTRPKKTRSRKEKDELEEILVIEG 464
              | :     | :  : |   :||| | ||| :   :||| :|: :||:| ||||
Db        434 IRKTTAG---KVNTASIAPVTKVFPLAKLDRAISFSITRPASSRTTQEKNEQEEILTFNK 490

Qy        465 IELERDHGHVKFDVYINADE----DDLAVISPENAEFAGSFVSLWHKPIKGKRTK---TQ 517
              :  : |  :|:|||::| |:    |:|     : ||||||: || |  : |  |    :
Db        491 VAYD-DTKYVRFDVFLNVDKTVNADEL-----DKAEFAGSYTSLPH--VHGNNTNHVTSV 542

Qy        518 LLTLSICDILEDLDADEDDYVLVTLVPRNAGDAIKIHNVKIELD 561
               |:| ::|||   :::| : |||||:  |: : | :|:|:|:
Db        543 TFKLAITELLEDNGLEDEDTIAVTLVPKVGGEGVSIESVEIKLE 586


Search completed: April  8, 2005, 21:37:21
Job time : 51 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2005, 19:44:53 ; Search time 263 Seconds
(without alignments)
3496.530 Million cell updates/sec

Title: US-09-446-089E-2
Perfect score: 2991
Sequence: 1 MFKNPNIRYHKLSSKSNDND.....VPRNAGDAIKIHNVKIELDG 562

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09446089/runat_07042005_163922_11867/app_query.fasta_1.711
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1560.5	52.2	1989	4	US-09-889-463A-19	Sequence 19, Appl
2	1539.5	51.5	2044	4	US-09-889-463A-27	Sequence 27, Appl
3	1539.5	51.5	2181	4	US-09-443-067-19	Sequence 19, Appl
4	1520.5	50.8	2485	4	US-09-889-463A-9	Sequence 9, Appli
5	1477	49.4	1990	4	US-08-482-934A-1	Sequence 1, Appli
6	1309	43.8	2260	4	US-09-889-463A-35	Sequence 35, Appl
7	1292	43.2	1993	4	US-09-889-463A-13	Sequence 13, Appl
8	1254	41.9	1994	4	US-09-889-463A-31	Sequence 31, Appl
9	1240.5	41.5	1522	4	US-09-443-067-25	Sequence 25, Appl
10	1160.5	38.8	1761	3	US-08-481-190-1	Sequence 1, Appli
11	1160.5	38.8	1761	5	PCT-US93-00869-1	Sequence 1, Appli
12	1147.5	38.4	2145	3	US-09-078-862-1	Sequence 1, Appli
13	1147.5	38.4	2146	4	US-09-866-153-11	Sequence 11, Appl
14	1147.5	38.4	2146	4	US-09-693-467A-11	Sequence 11, Appl
15	1147.5	38.4	2146	4	US-09-270-976-11	Sequence 11, Appl
16	1133.5	37.9	1764	3	US-08-481-190-14	Sequence 14, Appl
17	1133.5	37.9	1764	5	PCT-US93-00869-14	Sequence 14, Appl
18	1120	37.4	1788	3	US-08-481-190-5	Sequence 5, Appli
19	1120	37.4	1788	5	PCT-US93-00869-5	Sequence 5, Appli
20	1119.5	37.4	1749	3	US-08-481-190-17	Sequence 17, Appl
21	1119.5	37.4	1749	5	PCT-US93-00869-17	Sequence 17, Appl
22	1081.5	36.2	2057	4	US-09-443-067-29	Sequence 29, Appl
23	1014.5	33.9	2028	4	US-09-889-463A-33	Sequence 33, Appl
24	1003.5	33.6	1319	4	US-09-443-067-17	Sequence 17, Appl
25	974	32.6	2078	4	US-09-443-067-21	Sequence 21, Appl
26	861	28.8	1315	4	US-08-482-934A-11	Sequence 11, Appl
27	844	28.2	1325	4	US-08-482-934A-9	Sequence 9, Appli
28	806.5	27.0	670	4	US-09-443-067-15	Sequence 15, Appl
29	794.5	26.6	662	3	US-09-129-030-35	Sequence 35, Appl
30	794	26.5	852	4	US-09-889-463A-15	Sequence 15, Appl
31	775	25.9	988	4	US-09-889-463A-25	Sequence 25, Appl
32	773.5	25.9	2173	4	US-09-889-463A-39	Sequence 39, Appl
33	766.5	25.6	671	3	US-09-129-030-29	Sequence 29, Appl
34	762	25.5	689	3	US-09-129-030-33	Sequence 33, Appl
35	724.5	24.2	925	4	US-09-443-067-5	Sequence 5, Appli
36	722.5	24.2	960	4	US-09-443-067-7	Sequence 7, Appli
37	713.5	23.9	590	3	US-09-129-030-11	Sequence 11, Appl
38	709	23.7	667	3	US-09-129-030-25	Sequence 25, Appl
39	705	23.6	588	3	US-09-129-030-27	Sequence 27, Appl
40	701	23.4	582	4	US-09-443-067-1	Sequence 1, Appli
41	695	23.2	875	4	US-09-443-067-27	Sequence 27, Appl
42	691	23.1	674	3	US-09-129-030-23	Sequence 23, Appl
43	685.5	22.9	668	3	US-09-129-030-31	Sequence 31, Appl
44	674.5	22.6	590	3	US-09-129-030-1	Sequence 1, Appli
45	674	22.5	673	4	US-09-443-067-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-889-463A-19
; Sequence 19, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-19

Alignment Scores:

Pred. No.:	7.06e-176	Length:	1989
Score:	1560.50	Matches:	310
Percent Similarity:	70.99%	Conservative:	84
Best Local Similarity:	55.86%	Mismatches:	134
Query Match:	52.17%	Indels:	27
DB:	4	Gaps:	13

US-09-446-089E-2 (1-562) x US-09-889-463A-19 (1-1989)

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Qy         17 AsnAspAsnAspGln---GluSerSerHisArgCysLysHisIleLeuLeuPheIleIle 35
              |||  |||  |||  |||      |||      |||           ::::::
Db        179 AACCCTAATTCCCAGGGAGAACCTCCACATATTGTAGGACATAGGAGGAACGTTCTACTT 238
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Qy        36 ThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeuAlaTyrAlaArgPhe 55
Db       239 GGCCTAGGAGGGCTTTGTGGTGCTGTTACTCTTAACAACAACAACCCTTTTGCC---TTT 295

Qy        56 AlaSerThrSerThrGlyProIleAlaAlaProAspValThrLysCysGlyGlnProAsp 75
Db       296 GCAGCT-----------CCAATATCTCCTCCTGACCTAAACACGTGCGGTCCACCAGAC 343

Qy        76 LeuProProGlyThrAlaProIleAsnCysCysProProIleProAlaLysIleIleAsp 95
Db       344 CTACCCGCAGGTGTAAAACCCACCAATTGTTGCCCCCCA---TCTTCCAAAATCATAGAT 400

Qy        96 PheGluLeuProProProSerThrThrMetArgValArgArgAlaAlaHisLeuValAsp 115
Db       401 TTCAAGTTCTCTCCCTCTAACCAACCCTTGAGGGTAAGACCAGCCGCACATTTGGTCAAC 460

Qy       116 AspAlaTyrIleAlaLysPheLysLysAlaValGluLeuMetArgAlaLeuProGluAsp 135
Db       461 GATGAGTATCTAGCCAAATACAAAAAAGCCCTTGACCTCATGAAAAAACTCCCCTCTGAT 520

Qy       136 AspProArgSerPheLysGlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyr 155
Db       521 GACCCGCGTAATTTCACCCAACAAGCCAACGTTCATTGTGCTTATTGTGATGGTGCATAT 580

Qy       156 AsnGlnAlaGlyPheThrAsnLeuLysLeuGlnIleHisArgSerTrpLeuPhePhePro 175
Db       581 CACCAAGTTGGGTTCCCTGACCTCGATCTCCAAGTCCACAACTCCTGGCTCTTCTTCCCT 640

Qy       176 PheHisArgTyrTyrIleTyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThr 195
Db       641 TTCCATCGTTGGTATCTTTATTTCTATGAAAGGATCTTGGGGAGCTTGATCAATGATCCA 700

Qy       196 ThrPheAlaLeuGlnPheTrpAsnTyrAspSerProGlyGlyMetThrIleProSerMet 215
Db       701 ACCTTTGCCCTTCCATTTTGGAACTGGGATGCTCCTAAGGGCATGCAACTTCCTTCCATT 760

Qy       216 PheIleAspThrAsnSerSerLeuTyrAspSerLeuArgAspSerAsnHisGlnProPro 235
Db       761 TACGCAGACCCTAAATCACCCCTTTATGACACTCTCCGCAATGCCAATCATCAACCCCCA 820

Qy       236 ThrIleValAspLeuAsnTyrAlaPheSerAspSerAspAsnThrThrThrProGluGlu 255
Db       821 ACACTCGTAGACCTCGACTTCAATCTCGAGGAT------------CCTATTTCCAATGGC 868

Qy       256 GlnMetIleIleAsnLeuLysIleValTyrArgGlnMetValSerSerAlaLysThrPro 275
Db       869 AAAATTTCCAACAACCTCACCATAATGTATAGGCAAGTTGTGTCTAACGGGAAGACTCCT 928

Qy       276 GlnLeuPhePheGlyArgProTyrArgArgGlyAspGlnGluPheProGlyValGlySer 295
Db       929 ACATTGTTCCTTGGAAATCCTTACCGTGCTGGGGATGAGCCTGACCCGGGTTTTGGATCA 988

Qy       296 IleGluLeuValProHisGlyMetIleHisLeuTrpThrGlySerGluAsnThrProTyr 315
Db       989 GTAGAGAATGTTCCACATGGCCCTGTTCATCTTTGGACCGGTGATATCAACCAACCTAAC 1048

Qy       316 GlyGluAsnMetGlyAlaPheTyrSerThrAlaArgAspProIlePhePheAlaHisHis 335
Db      1049 ATTGAGAACATGGGAACTTTCTATTCAGCTGCAAGAGACCCCATTTTTTATTCTCATCAT 1108

Qy       336 SerAsnValAspArgMetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThrAsp 355
Db      1109 TCAAACATTGATAGGATGTGGTCCATATGGAAAACACTTGGTGGGAAAAGAAGG---GAT 1165

Qy       356 LeuThrAspProAspPheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGluMet 375
Db      1166 TTTACTGATTCAGATTGGTTAGAATCTGCGTTTCTCTTCTACGATGAGAACAAGAACCTT 1225

Qy       376 ValArgValLysValArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGlnAsp 395
Db      1226 GTGCGTGTGAAGGTCAAGGATTCTCTTGACACTAGAAAACTAGGGTATGTTTACCAAGAT 1285

Qy       396 ValGluIleProTrpLeuAsnThrArgProThrProLysValSer----------Pro 411
Db      1286 GTTGACATTCCATGGTTAAATTCTAAGCCCACGCCGCGTAGGTCAAGGGTTCAGAAGGTA 1345

Qy       412 SerLeuLeuLysLysPhe--------------HisArgThrAsnThrAlaAsnProArg 426
Db      1346 GCATTAGCACAAAATTTTGGTGTTGGTGCAGCACATGCTGCTGAGACTTCA------AGG 1399

Qy       427 GlnVal---PheProAlaIleLeuAspArgValLeuLysValIleValThrArgProLys 445
Db      1400 AATGTGAAGTTCCCACTAGTGTTGGATTCAGTTGTGAGCACAATGGTTAAAAGGCCAAAC 1459

Qy       446 LysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIleGluGlyIle 465
Db      1460 AAGTCGAGGAGCAAGAAGGAGAAGGAAGAGGAGGAAGAGGTTTTGGTGATTGAAGGGATT 1519

Qy       466 GluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAlaAspGluAsp 485
Db      1520 GAGTTTGAGAGA---AACACACCTGTGAAATTTGATGTGTTTATCAAT---GATGAAGAT 1573

Qy       486 AspLeuAlaValIleSerProGluAsnAlaGluPheAlaGlySerPheValSerLeuTrp 505
Db      1574 GAT---AAGCAGATTCGACCAGATAATACAGAATTTGCAGGAAGCTTTGTGAGTGTGCCT 1630

Qy       506 HisLysProIleLysGlyLysArgThrLysThrGlnLeuLeuThrLeuSerIleCysAsp 525
Db      1631 CATTCACATATGCACAAAAACAAGGACATCATTACTTGTTTGAGGCTGGGACTTACGGAT 1690

Qy       526 IleLeuGluAspLeuAspAlaAspGluAspAspTyrValLeuValThrLeuValProArg 545
Db      1691 TTGTTGGAAGAATTGGAAGCGGAAGATGATGACAGTGTTAGGGTGACGCTGGTTCCGAGA 1750

Qy       546 AsnAlaGlyAspAlaIleLysIleHisAsnValLysIleGluLeu 560
Db      1751 TATGGGAAAGGGCGTGTTAAAATCAGAGGCATCAAAATAGAGCTT 1795
```

RESULT 2
US-09-889-463A-27
; Sequence 27, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 2044
; TYPE: DNA
; ORGANISM: Glycine max
US-09-889-463A-27

Alignment Scores:

Pred. No.:	2.41e-173	Length:	2044
Score:	1539.50	Matches:	306
Percent Similarity:	67.99%	Conservative:	87
Best Local Similarity:	52.94%	Mismatches:	146
Query Match:	51.47%	Indels:	39
DB:	4	Gaps:	14

US-09-446-089E-2 (1-562) x US-09-889-463A-27 (1-2044)

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Qy         2 PheLysAsnProAsnIleArgTyrHisLysLeuSerSerLysSerAsnAspAsnAspGln 21
Db       111 TATCGAAAACCAAAACGCCATCATCATATTCCTAGAGTGACATGCAGTGACAACCAAAAA 170
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Qy        22 GluSerSer--------------------HisArgCysLysHisIleLeuLeuPheIle 34
Db       171 CCAAACACATCTGGAGAACTAGTACTCCCACATAGG---AGGAACATTCTACTTGGCCTA 227

Qy        35 IleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeuAlaTyrAlaArg 54
Db       228 GGAGGGCTTTGTGGTGCTGCTGCTACTCTT---------AACAACATCCCTTTTGCCAAT 278

Qy        55 PheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLysCysGlyGlnPro 74
Db       279 GCTGCC--------------CCAATACTTGGTCCAGACCTAACCACATGTGTTCAAGCA 323

Qy        75 AspLeuProProGlyThrAlaProIleAsnCysCysProProIleProAlaLysIleIle 94
Db       324 GAACTACCCGAAGGTGTAGAACCCACCAATTGTTGTCCCCCAATTTCCACAAACATCATA 383

Qy        95 AspPheGluLeuProProProSerThrThrMetArgValArgArgAlaAlaHisLeuVal 114
Db       384 GATTTCAAGTTCCCTCCCTCCAACCAACCCTTGCGTGTACGATCCGCTGCTCATCTGGTC 443

Qy       115 AspAspAlaTyrIleAlaLysPheLysLysAlaValGluLeuMetArgAlaLeuProGlu 134
Db       444 AACAAAGACTATCTAGCTAAATACGAGAAAGCCGTTAACCTGATGAAAAATCTCCCGTCA 503

Qy       135 AspAspProArgSerPheLysGlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAla 154
Db       504 GATGATCCACGTAGTTTCGCGCAACAAGCCAAAGTTCATTGTGCTTATTGCGACGGTGGA 563

Qy       155 TyrAsnGlnAlaGlyPheThrAsnLeuLysLeuGlnIleHisArgSerTrpLeuPhePhe 174
Db       564 TATCACCAACTAGGCTTCCCTGACCTTGATCTCGAAGTGCACTTCTCTTGGCTCTTCTTT 623

Qy       175 ProPheHisArgTyrTyrIleTyrPhePheGluArgIleLeuGlyLysLeuIleAsnAsp 194
Db       624 CCTTACCACAGATGGTATCTCTATTTCCATGAAAGGATATTGGCGAGCTTGATCAATGAT 683

Qy       195 ThrThrPheAlaLeuGlnPheTrpAsnTyrAspSerProGlyGlyMetThrIleProSer 214
Db       684 CCAACCTTTGCTCTTCCATTTTGGAACTGGGATGCTCCTGGGGGCATGCAACTTCCTTCC 743

Qy       215 MetPheIleAspThrAsnSerSerLeuTyrAspSerLeuArgAspSerAsnHisGlnPro 234
Db       744 ATGTACGCAGATCCCAAATCACCCCTTTATGATTCTCTACGCAATGCCAACCATCAACCA 803

Qy       235 ProThrIleValAspLeuAsnTyrAlaPheSerAspSerAspAsnThrThrThrProGlu 254
Db       804 CCAACACTTGTAAACCTTGACTTTACTATCGAGGATCCTAAT------------GCAGAG 851

Qy       255 GluGlnMetIleIleAsnLeuLysIleValTyrArgGlnMetValSerSerAlaLysThr 274
Db       852 GCAAATATCTCCACCAACCTCACCACAATGTATAGGCAGCTTGTGTCTAACGCAAAGACT 911

Qy       275 ProGlnLeuPhePheGlyArgProTyrArgArgGlyAspGlnGluPheProGlyValGly 294
Db       912 CCAACATTGTTCTTCGGAAATCCTTATCGTGCTGGGGATCAGCCTAACCCTGGTGGTGGC 971

Qy       295 SerIleGluLeuValProHisGlyMetIleHisLeuTrpThrGlySerGluAsnThrPro 314
Db       972 TCCGTAGAGAGCACTCCACATGGTCCTGTTCATGCATGGACCGGTGATATCAACCACCCT 1031

Qy       315 TyrGlyGluAsnMetGlyAlaPheTyrSerThrAlaArgAspProIlePhePheAlaHis 334
Db      1032 ACAATGGAGGACATGGGGAATTTATATGCAGCTGCAAGAGACCCCATTTTCTATTGCCAC 1091

Qy       335 HisSerAsnValAspArgMetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThr 354
Db      1092 CATTCCAATGTTGATAGGATGTGGTCCATATGGAAAACACTTGGTGGGAAAAGAAGG--- 1148

Qy       355 AspLeuThrAspProAspPheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGlu 374
Db      1149 GATTTAACAGACCCGGATTGGTTAGAATCCGCGTTTCTCTTCTACGATGAGAATAAGAAC 1208

Qy       375 MetValArgValLysValArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGln 394
Db      1209 CTTGTGCGTGTGAAGACTAAGGATTGTCTTGACACGAGAAAGTTAGGGTATGTTTACCAA 1268

Qy       395 AspValGluIleProTrpLeuAsnThrArgProThrPro---------------------- 407
Db      1269 GATGTTGACATTCCATGGTTAAAATCTAAGCCTACGCCATTAAGGTCAAGGGCTCAAAAG 1328

Qy       408 ---LysValSerProSerLeu------LeuLysLysPheHisArgThrAsnThrAlaAsn 424
Db      1329 GTAGAACTGACACCACTTTTTGGTGGTGTTGCTGCAGCACATGCTGCTGAGACTTCA--- 1385

Qy       425 ProArgGlnVal---PheProAlaIleLeuAspArgValLeuLysValIleValThrArg 443
Db      1386 ---AGGAATGTGAAGTTCCCATTGGTGTTGGATTCAGTTGTGAGTACAGTGGTGAAGAGG 1442

Qy       444 ProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIleGlu 463
Db      1443 CCAAAGAAGTCTAGGAGCAAAAAGGAGAAGGAAGAGAAGGAGGAGATTCTGGTGGTTGAA 1502

Qy       464 GlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAlaAsp 483
Db      1503 GGGATTGAGTTTGAGAGCAGCACAGGT---GTGAAGTTTGATGTGTTTATTAAT---GAT 1556

Qy       484 GluAspAspLeuAlaValIleSerProGluAsnAlaGluPheAlaGlySerPheValSer 503
Db      1557 GAAGATGAT---AAGTTGGTCAAGCCAGATAATACGGAGTTTGCAGGAAGCTTTGTGAGT 1613

Qy       504 LeuTrpHisLysProIleLysGlyLysArgThrLys------ThrGlnLeuLeuThrLeu 521
Db      1614 GTGCCTCATTCGCATGAGCATCACAAAAACAACAAGAAGATTGTTACTTGTTTGAGGTTG 1673

Qy       522 SerIleCysAspIleLeuGluAspLeuAspAlaAspGluAspAspTyrValLeuValThr 541
Db      1674 GGACTAACGGATTTGTTGGAAGAATTGGGAGCAGAAGATGATGATAGTGTTCTAGTAACA 1733

Qy       542 LeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsnValLysIleGlu 559
Db      1734 TTGGTTCCCAAGTATGGGAAAGGGCGAGTTAACATCAGAGGCATCAAGATAGAT 1787
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RESULT 3
US-09-443-067-19
; Sequence 19, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976, 222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: pineapple
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1858)
US-09-443-067-19

Alignment Scores:

Pred. No.:	2.69e-173	Length:	2181
Score:	1539.50	Matches:	305
Percent Similarity:	68.41%	Conservative:	87
Best Local Similarity:	53.23%	Mismatches:	155
Query Match:	51.47%	Indels:	26
DB:	4	Gaps:	10

US-09-446-089E-2 (1-562) x US-09-443-067-19 (1-2181)

```
Qy          3 LysAsnProAsnIleArgTyrHisLysLeuSerSerLysSerAsnAspAsnAspGlnGlu 22
Db        163 AGGGGTCCCAAACCACCCCGTCATAAGATCTCATGCAAATCTAAGGAGCAACAAGAGAAT 222

Qy         23 SerSerHisArgCysLysHisIleLeuLeuPheIleIleThrLeuPheLeu-LeuIleVa 42
Db        223 GCCGACAAGCCTGCGGGCCGCATCGCCCGC------CGCGACCTACTCCTGGGCCCTCGG 276

Qy         42 lGlyLeuTyrIleAlaAsnSer---LeuAlaTyrAlaArgPheAlaSerThrSerThrGl 61
Db        277 CGGGCTTTACGGTGCCACCACTGGGCTCGGCCTCAACCGTCGAGCGGCCGCCGCC----- 331

Qy         61 yProIleAlaAlaProAspValThrLysCysGlyGlnPro---AspLeuProProGlyTh 80
Db        332 -CCTATCCTGGCTCCCGACCTCTCAACTTGTGGGCCGCCTGCCGACCTCCCTGCCTCCGC 390

Qy         80 rAlaProIleAsnCysCysProProIleProAlaLysIleIleAspPheGluLeuProPr 100
Db        391 CCGACCGACAGTTTGCTGCCCGCCATACCAATCCACCATCATCGACTTCAAGCTCCCCCC 450

Qy        100 oProSerThrThrMetArgValArgArgAlaAlaHisLeuValAspAspAlaTyrIleAl 120
Db        451 GCGATCTGCTCCGCTTCGCGTCCGGCCTGCGGCCCACTTGGTTGACGCCGACTACCTGGC 510

Qy        120 aLysPheLysLysAlaValGluLeuMetArgAlaLeuProGluAspAspProArgSerPh 140
Db        511 CAAGTATAAGAAGGCGGTCGAGCTCATGAGGGCCCTGCCGGCCGACGACCCGCGCAACTT 570

Qy        140 eLysGlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPh 160
Db        571 CGTACAGCAAGCGAAAGTGCACTGTGCGTATTGCGACGGCGCGTATGACCAAATCGGCTT 630

Qy        160 eThrAsnLeuLysLeuGlnIleHisArgSerTrpLeuPheProPheHisArgTyrTy 180
Db        631 CCCCGATCTCGAGATCCAGATCCACAACTCGTGGCTCTTCTTTCCTTGGCACCGGTTCTA 690

Qy        180 rIleTyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGl 200
Db        691 CCTCTACTCCAACGAGCGCATACTCGGGAAACTTATCGGCGACGACACGTTCGCGCTGCC 750

Qy        200 nPheTrpAsnTyrAspSerProGlyGlyMetThrIleProSerMetPheIleAspThrAs 220
Db        751 TTTCTGGAACTGGGACGCGCCGGGGGGCATGCAGTTCCCGTCTATCTACACAGACCCTTC 810

Qy        220 nSerSerLeuTyrAspSerLeuArgAspSerAsnHisGlnProProThrIleValAspLe 240
Db        811 ATCCTCGCTATATGACAAGCTGCGTGATGCGAAGCACCAGCCGCCGACTTTGATTGACCT 870

Qy        240 uAsnTyrAlaPheSerAspSerAspAsnThrThrThrProGluGluGlnMetIleIleAs 260
Db        871 CGACTAC------AATGGCACCGATCCTACCTTCTCCCCTGAAGAACAGATTAACCACAA 924

Qy        260 nLeuLysIleValTyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGl 280
Db        925 CCTCGCCGTCATGTACCGACAGGTGATATCCAGTGGAAAGACGCCAGAGCTGTTTATGGG 984

Qy        280 yArgProTyrArgArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValPr 300
Db        985 CTCAGCGTACCGCGCCGGTGACCAGCCTGACCCCGGCGCAGGCTCTGTAGAGCAGAAGCC 1044

Qy        300 oHisGlyMetIleHisLeuTrpThrGlySerGluAsnThrProTyrGlyGluAsnMetGl 320
Db       1045 GCACGGCCCGGTGCATGTGTGGACAGGTGATCGCAACCAGCCCAATCGCGAAGACATGGG 1104

Qy        320 yAlaPheTyrSerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspAr 340
Db       1105 CACGCTCTACTCGGCGGCGTGGGACCCCGTCTTCTTCGCACACCACGGCAACATCGACCG 1164

Qy        340 gMetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAs 360
Db       1165 CATGTGGTACGTGTGGAGGAACCTTGGCGGCAAGCACCGC---AACTTCACCGACCCCGA 1221

Qy        360 pPheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysVa 380
Db       1222 CTGGCTCAACGCGTCCTTCCTGTTCTATGATGAGAATGCGCAGCTCGTCCGTGTTAAAGT 1281

Qy        380 lArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTr 400
Db       1282 AAAAGACTGCTTAGAGGCCGACGCAATGCGGTACACATACCAGGATGTAGAGATCCCGTG 1341

Qy        400 pLeuAsnThrArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgTh 420
Db       1342 GCTCAAAGCAAAGCCGACGCCAAAGAGCGCCCTACAGAAGATAAAGAGCAAGGTATCGAC 1401

Qy        420 rAsnThrAlaAsnProArg----------------------GlnValPheProAlaIl 432
Db       1402 GCTGAAGGCAACACCAAGGGGGACGACGACTACCACAGCAGAGACTACATTTCCGGTGGT 1461

Qy        432 eLeuAspArgValLeuLysValIleValThrArgProLysLysThrArgSerArgLysGl 452
Db       1462 GCTGGATAAGCCGGTGAGTGCAACAGTGGCTAGACCGAAGGCCAGGAGGAGTGGGAAGGA 1521

Qy        452 uLysAspGluLeuGluGluIleLeuValIleGluGlyIleGluLeuGluArgAspHisGl 472
Db       1522 GAAGGAAGAAGAGGAGGAGGTGTTGGTGGTGGAGGGAATCGAGTTGGAGAAGGAC---GT 1578

Qy        472 yHisValLysPheAspValTyrIleAsnAlaAspGluAspAspLeuAlaValIleSerPr 492
Db       1579 GTTCGTGAAGTTTGATGTGTATATAAACTCGCCGGAGCACGAA------GGGGTGGGGCC 1632

Qy        492 oGluAsnAlaGluPheAlaGlySerPheValSerLeuTrpHisLysProIleLysGlyLy 512
Db       1633 GGAGGCGAGTGAGTTCGCAGGGAGCTTCGTCCACGTGCCACACAAGCACAAGAAGGCGAA 1692

Qy        512 sArgThrLysThrGlnLeu--------------LeuThrLeuSerIleCysAspIleLe 527
Db       1693 GAAGGGGAAGGAGATGGCCAGGATGAACACAAGGCTTAAGCTCGGGATAACGGACCTGCT 1752

Qy        527 uGluAspLeuAspAlaAspGluAspAspTyrValLeuValThrLeuValProArgAsnAl 547
Db       1753 CGAGGACATCGGCGCTGAGGACGACGAGAGCGTGCTCATCACGCTCGTGCCCAGGAGCGG 1812

Qy        547 aGlyAspAlaIleLysIleHisAsnValLysIleGlu 559
Db       1813 CAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTGAT 1849
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RESULT 4
US-09-889-463A-9
; Sequence 9, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio C.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
; FILE REFERENCE: BB1330
; CURRENT APPLICATION NUMBER: US/09/889,463A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/119,590
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 2485
; TYPE: DNA
; ORGANISM: Glycine max

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US-09-889-463A-9

Alignment Scores:
Pred. No.:              6.29e-171       Length:         2485
Score:                  1520.50         Matches:        289
Percent Similarity:     71.59%          Conservative:   84
Best Local Similarity:  55.47%          Mismatches:     125
Query Match:            50.84%          Indels:         23
DB:                     4               Gaps:           9

US-09-446-089E-2 (1-562) x US-09-889-463A-9 (1-2485)

Qy         48 AsnSerLeuAlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAsp 67
Db        363 AACCCTTTTGCATTTGCT--------------------GCGCCAATATCTCCTCCAGAC 401

Qy         68 ValThrLysCysGlyGlnProAspLeuProProGlyThrAlaProIleAsnCysCysPro 87
Db        402 CTAACCACATGTGGTCCACCAGACCTACCTGAAGGTGCAGAACCCACAAATTGTTGCCCC 461

Qy         88 ProIleProAlaLysIleIleAspPheGluLeuProProProSerThrThrMetArgVal 107
Db        462 CCATTTTCATCCACCATCATAGATTTCAAGTTTCCTCCTTCTAACAAACCTTTGCGTGTA 521

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
Db        522 AGACCAGCTGCACATTTAGTTGACAAAAATTATCTAGCCAAATACAAAAAAGCCATTGAC 581

Qy        128 LeuMetArgAlaLeuProGluAspAspProArgSerPheLysGlnGlnAlaAsnValHis 147
Db        582 CTCATGAAAAAACTCCCAGCTAACGATCCACGCAATTTCATGCAACAAGCAAACGTGCAC 641

Qy        148 CysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeuGlnIle 167
Db        642 TGCGCTTATTGCACTGGTTCATATGACCAAGTTGGGTTCCCTGGCCTTGAGCTCCAAGTG 701

Qy        168 HisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGluArgIle 187
Db        702 CACAGCTCTTGGCTCTTCTTTCCCTACCACCGATGGTTCCTCTATTTCTATGAGAGAATT 761

Qy        188 LeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAspSerPro 207
Db        762 TTGGGGAGCTTGATCAATGATCCAACATTTGCCCTTCCATTTTGGAACTGGGATGCTCCT 821

Qy        208 GlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAspSerLeu 227
Db        822 AAGGGCATGCAACTTCCTTCCATTTATGCAGACCCCAAATCACCTCTTTATGACCCTCTT 881

Qy        228 ArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSerAspSer 247
Db        882 CGCAATGCGAATCACCAACCTCCAACACTTGTGGACTTTGACTTC---------AATCTT 932

Qy        248 AspAsnThrThrThrProGluGluGlnMetIleIleAsnLeuLysIleValTyrArgGln 267
Db        933 GACAATCCTATTTCC---AATGGAAGAATCTCCACCAACCTCACCATAATGTATAGGCAA 989

Qy        268 MetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArgArgGlyAsp 287
Db        990 CTTGTGTCTAATGGAAAAACTCCTACTTTGTTCCTTGGAAATCCTTATCGTGCCGGGGAT 1049

Qy        288 GlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIleHisLeuTrp 307
Db       1050 GCGCCTGACCCTGGCGGTGGCTCAGTAGAGGGCGTTCCACATGGTCCGGTTCATCTATGG 1109

Qy        308 ThrGlySerGluAsnThrProTyrGlyGluAsnMetGlyAlaPheTyrSerThrAlaArg 327
Db       1110 ACAGGTGATATAAATCAACCAAACATTGAGAACATGGGGGATTTCTATTCTGCTGCAAGA 1169

Qy        328 AspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSerIleTrpLysThr 347
Db       1170 GATCCTATTTTCTATTCTCACCATTCCAATGTTGATAGGATGTGGTCTATATGGAAAACA 1229

Qy        348 LeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAspAlaSerPheVal 367
Db       1230 CTTGGTGGGAAGAGAAGG---GATTTCACCGACTCAGATTGGTTGGAATCTGGGCTCCTC 1286

Qy        368 PheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCysLeuAspGluLys 387
Db       1287 TTCTACGATGAGAATAAGAACCTTGTGCGTGTGAAGGTCAAGGATTGTCTTGACACAAGA 1346

Qy        388 LysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThrArgProThrPro 407
Db       1347 AAGCTAGGATATGTTTACCAAGATGTTGAAATTCCATGGTTAAAATCTAAGCCTTCACCG 1406

Qy        408 ---------LysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAlaAsn 424
Db       1407 CGTAGGTCGAGGGTTCAAAAGGTAGCACTAGGACCACATTTTAATACTGGTGTAGCACGT 1466

Qy        425 ProArgGlnVal--------------PheProAlaIleLeuAspArgValLeuLysVal 439
Db       1467 GCTGCTGAGACTTCGAGGAATGTTCAGTTCCCATTGGTGTTGGATTCAGTTGTGAGCATA 1526

Qy        440 IleValThrArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIle 459
Db       1527 GTGGTGAAGAGGCCAAAAAAGTCGAGGAGCAAGAAGGAGAAGGAAGAGGAAGAGGAGGTT 1586

Qy        460 LeuValIleGluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyr 479
Db       1587 CTTGTGATTGAAGGGGTTGAGTATGAC---AGCAACATACCAGTGAAATTTGATGTGCTT 1643

Qy        480 IleAsnAlaAspGluAspAspLeuAlaValIleSerProGluAsnAlaGluPheAlaGly 499
Db       1644 ATTAAT---GATGAAGATGAT---AAGCAGATTCAGCCAGAAGATTCGGAGTATGCAGGA 1697

Qy        500 SerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLysThrGlnLeuLeu 519
Db       1698 AGCTTTGTGACTGTGCCTCATTCGCATAAGCACAAAAATAAGAAGATTATCACTTGTTTG 1757

Qy        520 ThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAspAspTyrValLeu 539
Db       1758 AGGCTGGGACTGACAGATTTGTTGGAAGAATTGGAAGCAGAAGATGATGATAGTGTTGTG 1817

Qy        540 ValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsnValLysIleGlu 559
Db       1818 GTGACGTTGGTTCCGAGGTATGGGAAAGGGCGTGTCCAAATTGGAGGCATCAAGATAGAT 1877

Qy        560 Leu 560
Db       1878 CTT 1880

RESULT 5
US-08-482-934A-1
; Sequence 1, Application US/08482934A
; Patent No. 6703542
;  GENERAL INFORMATION:
;    APPLICANT:  Robinson, Simon P.
;    APPLICANT:  Dry, Ian B.
;    TITLE OF INVENTION:  Polyphenol Oxidase Genes
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,934A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/182,045
;      FILING DATE:  14-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/AU92/00356
;      FILING DATE:  16-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PK7248
;      FILING DATE:  17-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John P. White
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  51461-Z/JPW/GJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  GPO1 cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..1848
US-08-482-934A-1

Alignment Scores:
Pred. No.:                6.9e-166      Length:          1990
Score:                    1477.00       Matches:         287
Percent Similarity:       68.65%        Conservative:    105
Best Local Similarity:    50.26%        Mismatches:      139
Query Match:              49.38%        Indels:          40
DB:                       4             Gaps:            12

US-09-446-089E-2 (1-562) x US-08-482-934A-1 (1-1990)

Qy          4 AsnProAsnIleArgTyrHisLysLeuSerSerLysSerAsnAspAsnAspGlnGluSer 23
              :::||||||                  |||      ::::::|||      :::   |||
Db        199 GATCCCAAC-----------------TCGGATTCTACCTCCGACGTTCGAGAAACTTCC 240

Qy         24 SerHisArgCys------LysHisIleLeuLeuPheIleIleThrLeuPheLeuLeuIle 41
              |||   :::         :::::::::||||||   |||       |||:::
Db        241 TCAGGGAAGTTAGATAGGAGGAATGTGCTTCTTGGCATAGGAGGGCTGTATGGTGCTGCT 300

Qy         42 ValGlyLeuTyrIleAlaAsnSerLeuAlaTyrAlaArgPheAlaSerThrSerThrGly 61
              ||||||                  ||||||:::
Db        301 GGCGGTCTCGGCGCCACTAAGCCATTAGCCTTTGGG--------------------GCT 339

Qy         62 ProIleAlaAlaProAspValThrLysCysGlyGlnProAspLeuProProGlyThrAla 81
              ||||||   |||||||||::::::|||||||||          :::|||   |||
Db        340 CCCATCCAGGCACCGGATATATCCAAGTGTGGTACCGCCACCGTGCCTGATGGTGTAACG 399

Qy         82 ProIleAsnCysCysProProIleProAlaLysIleIleAspPheGluLeuProProPro 101
              |||   |||||||||||||||:::       |||||||||||||||:::||||||
Db        400 CCCACAAATTGCTGCCCGCCAGTCACCACAAAGATTATAGATTTCCAGCTACCTTCCTCA 459

Qy        102 SerThrThrMetArgValArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLys 121
                 :::   ||||||   |||   ||||||||||||||||          |||:::||||||
Db        460 GGTTCCCCCATGCGTACCAGGCCAGCTGCTCACTTGGTCAGCAAAGAGTACTTAGCCAAG 519

Qy        122 PheLysLysAlaValGluLeuMetArgAlaLeuProGluAspAspProArgSerPheLys 141
              :::||||||||||:::||||||   :::||||||||||:::||||||||||||||||||||
Db        520 TATAAAAAGGCCATTGAGCTGCAGAAAGCTCTTCCTGATGATGATCCGCGTAGTTTCAAG 579

Qy        142 GlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThr 161
              ||||||||||||||||||||   ||||||   ||||||||:::|||   |||:::|||
Db        580 CAACAGGCTAATGTCCATTGCACCTATTGCCAAGGGGCTTATGATCAGGTTGGGTATACC 639

Qy        162 AsnLeuLysLeuGlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIle 181
              :::|||:::||||||:::|||   ||||||||||||   ||||||||||||||||||:::
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Db        640 GACCTAGAACTCCAGGTTCATGCTTCATGGCTTTTCCTCCCTTTCCACCGTTACTATCTC 699

Qy        182 TyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPhe 201
              ||||||   ||||||||||||   |||||||||:::|||   ||||||||||||   :::
Db        700 TACTTCAATGAGAGAATTCTTGCAAAGTTGATCGACGATCCCACCTTCGCTTTGCCCTAT 759

Qy        202 TrpAsnTyrAspSerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSer 221
              |||   :::|||:::|||   ||||||   :::|||:::::::::      :::   |||
Db        760 TGGGCTTGGGATAACCCTGATGGCATGTATATGCCGACCATCTATGCTAGTTCCCCATCA 819

Qy        222 SerLeuTyrAspSerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsn 241
              ||||||||||||      |||::::::   |||   |||||||||:::::||||||:::
Db        820 TCACTCTACGACGAGAAGCGCAACGCCAAGCACCTGCCTCCGACTGTGATCGATCTCGAC 879

Qy        242 TyrAlaPheSerAspSerAspAsnThrThrProGluGluGlnMet---IleIleAsn 260
              |||          |||           |||   |||::::::::::::          |||
Db        880 TAC---------GATGGCACCGAACCCACAATCCCTGATGACGAACTAAAAACCGACAAT 930

Qy        261 LeuLysIleValTyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGly 280
              |||   |||:::|||:::|||:::||||||   |||   ||||||:::||||||   |||
Db        931 CTGGCAATCATGTACAAACAAATTGTGTCGGGTGCCACGACTCCTAAGCTTTTCCTTGGT 990

Qy        281 ArgProTyrArgArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValPro 300
                 |||||||||   ||||||          ||||||   |||::::::|||       |||
Db        991 TACCCATACCGCGCCGGCGATGCGATTGACCCTGGAGCGGGTACCCTTGAGCACGCCCCA 1050

Qy        301 HisGlyMetIleHisLeuTrpThrGlySerGluAsnThrProTyrGlyGluAsnMetGly 320
              |||   ::::::|||   |||||||||       :::   |||       |||:::||||||
Db       1051 CATAATATAGTCCACAAATGGACTGGTCTTGCTGATAAGCCT---AGTGAGGACATGGGA 1107

Qy        321 AlaPheTyrSerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArg 340
                 ||||||:::          ||||||||||||||||||   ||||||:::||||||||||
Db       1108 AACTTCTATACTGCCGGCAGAGACCCCATATTCTTCGGTCACCACGCCAATGTCGATCGG 1167

Qy        341 MetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAsp 360
              ||||||:::|||||||||||:::||||||      |||   |||   ||||||   |||
Db       1168 ATGTGGAATATATGGAAAACTATAGGAGGTAAAAATAGAAAGGATTTCACGGATACGGAT 1227

Qy        361 PheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysVal 380
              :::||||||||||:::||||||||||||||||||||||   ::::::|||:::||||||||
Db       1228 TGGCTTGACGCCACGTTCGTCTTCTACGACGAGAACAAACAACTTGTTAAAGTCAAGGTC 1287

Qy        381 ArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrp 400
              ||||||:::|||      ||||||   |||   |||||||||:::   |||||||||
Db       1288 TCGGACTGTGTCGACACTTCCAAGCTGAGATACCAATATCAGGATATTCCTATTCCATGG 1347

Qy        401 Leu------AsnThrArgProThrProLysValSerProSerLeuLeuLysLysPheHis 418
              |||      ||||||:::          |||   :::                |||
Db       1348 CTACCAAAAAATACGAAGGCCAAAGCGAAGACGACC------------ACCAAAAGTTCC 1395

Qy        419 ArgThrAsnThrAlaAsnProArgGlnVal---------------------------- 428
              ::::::      |||          ::::::
Db       1396 AAGTCGGGAGTAGCGAAAGCGGCCGAACTCCCAAAGACGACGATCAGCAGCATCGGAGAC 1455

Qy        429 PheProAlaIleLeuAspArgValLeuLysValIleValThrArgProLysLysThrArg 448
              ||||||      |||:::   |||::::::|||   |||   ||||||||||||:::|||
Db       1456 TTCCCAAAAGCTCTTAACTCAGTGATAAGAGTAGAAGTTCCAAGGCCAAAGAAATCAAGA 1515

Qy        449 SerArgLysGluLysAspGluLeuGluGluIleLeuValIleGluGlyIleGluLeuGlu 468
              |||:::|||||||||::::::   ||||||:::|||:::|||:::|||||||||||||:::
Db       1516 AGCAAGAAGGAGAAAAGAGGATGAGGAAGAGGTGTTACTGATAAAAGGAATAGAGCTAGAT 1575

Qy        469 ArgAspHisGlyHisValLysPheAspValTyrIleAsnAlaAspGluAspAspLeuAla 488
              |||::::::      ||||||||||||||||||||||||      :::::::|||   :::
Db       1576 AGAGAGAAT---TTCGTGAAGTTTGATGTGTACATCAAC------GACGAAGATTATTCA 1626

Qy        489 ValIleSerProGluAsnAlaGluPheAlaGlySerPheValSerLeuTrpHisLysPro 508
              |||      |||:::|||:::|||||||||||||||||||||::::::   ||||||
Db       1627 GTGAGTAGGCCTAAGAATAGTGAGTTTGCAGGAAGCTTTGTGAACGTACCACACAAGCAT 1686

Qy        509 IleLysGlyLysArgThrLysThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGlu 528
              :::|||      :::|||||||||      |||      :::|||   ::::::||||||
Db       1687 ATGAAAGAAATGAAGACGAAGACCAAT---CTGAGGTTCGCGATAAATGAGCTGTTAGAG 1743
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Qy        529 AspLeuAspAlaAspGluAspAspTyrValLeuValThrLeuValProArgAsnAlaGly 548
Db       1744 GACTTGGGAGCCGAAGATGATGAGAGTGTGATCGTGACTATAGTCCCTCGTGCTGGGGGC 1803

Qy        549 AspAlaIleLysIleHisAsnValLysIleGlu 559
Db       1804 GATGATGTCACCATTGGTGGAATTGAGATCGAG 1836

RESULT 6
US-09-889-463A-35
; Sequence 35, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
;   LENGTH: 2260
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-889-463A-35

Alignment Scores:
Pred. No.:              1.08e-145     Length:          2260
Score:                  1309.00       Matches:         258
Percent Similarity:     67.94%        Conservative:    81
Best Local Similarity:  51.70%        Mismatches:      146
Query Match:            43.76%        Indels:          14
DB:                     4             Gaps:            11

US-09-446-089E-2 (1-562) x US-09-889-463A-35 (1-2260)

Qy         67 AspValThrLysCysGlyGlnProAspLeuProPro---GlyThrAlaProIleAsnCys 85
Db        391 AATGTAAGCAAGTGTTTTCCCGTTGAGTTACCTTCTTTTGCAATAACCAATTCCCATTGT 450

Qy         86 CysPro------ProIleProAlaLysIleIleAspPhe---GluLeuProProProSer 102
Db        451 TGTCCACCTAGACCACCTCCTTCTAAGATCATAGATTTCAAAGATTTTGCTTCTCCAAAC 510

Qy        103 ThrThrMetArgValArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPhe 122
Db        511 GCCACGCTTCGAGTAAGAAAACCGGCTCACATGGTAGATGAGGAGTACATAGCAAAACTT 570

Qy        123 LysLysAlaValGluLeuMetArgAlaLeuProGluAspAspProArgSerPheLysGln 142
Db        571 GAAAAGGGCATTGCACTCATGAAAGCACTCCCTGATGATGACCCACGTAATTTCATACAA 630

Qy        143 GlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyrAsn---GlnAlaGlyPheThr 161
Db        631 CAAGCAAAGGTCCATTGTGCTTATTGTAACGGTGCCTATCACCTACCCCATCCCTTTCAG 690

Qy        162 AsnLeuLysLeuGlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIle 181
Db        691 AACACAAAACTCAACATTCACAGGTCTTGGTTTTTCTTTCCTTTCCACCGTTGGTACATT 750

Qy        182 TyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPhe 201
Db        751 TACTTCTTCGAGCGAATCTTGGGAAGCTTGCTCGGTGACCCGAACTTTGCCTTACCGTTT 810

Qy        202 TrpAsnTyrAspSerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSer 221
Db        811 TGGAATTGGGATGCTGTAGAAGGGATGCAAATGCCACCATATTTCGCAAACCCTAACTCG 870

Qy        222 SerLeuTyrAspSerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsn 241
Db        871 TCGCTCTATCACAAACTCCGAAACCCCAAGCACTTGCCACCGCAAGTGGTTGACCTGAAC 930

Qy        242 TyrAlaPheSerAspSerAspAsnThrThrThrProGluGluGlnMetIleIleAsnLeu 261
Db        931 TATGATCCATTTGACTTTAATGATGATACACCTTCTCATCAACAAGTTTCGTATAATCTA 990

Qy        262 LysIleValTyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArg 281
Db        991 GCCTTCATGTACAAGCAAATGGTG---CTAGCAAGTACCAAAGAATTGTTCATGGGAAGC 1047

Qy        282 ProTyrArgArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHis 301
Db       1048 CCTTTTCGACTCGGCGATAACCCTACTCCGGGTATTGGCTCTATAGAGGCTGCTCCTCAT 1107

Qy        302 GlyMetIleHisLeuTrpThrGlySerGluAsnThrProTyrGlyGluAsnMetGlyAla 321
Db       1108 AACACGGTTCATAAATGGGTTGGTGCTGCTGATAAGCCACACCAGGAGGACATGGGAACG 1167

Qy        322 PheTyrSerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMet 341
Db       1168 TTCTACACAGCTGCTAGAGATCCCGTTTTCTATCCGCATCACACGAACTCGGATCGACTG 1227

Qy        342 TrpSerIleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPhe 361
Db       1228 TGGGGGATATGGAAAAAATTGGGAGAAGGAAGAAAGGACTATAGTGATGATCCAGATTGG 1287

Qy        362 LeuAspAlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArg 381
Db       1288 TTAGATTCTGATTTTTACTTCTATGATGAGAATGCCAATTTTGTTCGCGTGAAGGTAAGA 1347

Qy        382 AspCysLeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeu 401
Db       1348 GATTGCTTTGATACTAAAAGATTGGGGTATGTTTACGAAGATGTTGATCTTCCATGGTTG 1407

Qy        402 AsnThrArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsn 421
Db       1408 CGAACGCCACCCACATCGCGAAAAAGCAAGCTACTAAGAGAAGCCAAAAAGGGTTCACTT 1467

Qy        422 ThrAlaAsnProArgGlnValPheProAlaIleLeuAspArgValLeuLysValIleVal 441
Db       1468 TTGAGTTCAAAGCCATGGAAATTTCCTTTGGTTTTGGATTCCATAACGAGTATTGTTGTT 1527

Qy        442 ThrArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuVal 461
Db       1528 AAGAGGCCGAAGAAATGGAGGAGCAAGGAGGAGAAAGAACAAGAGGAGGAGGTTTTGGTG 1587

Qy        462 IleGluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsn 481
Db       1588 ATAGAAGGGATTGAGTTTGGAAGTGATAAA---TATGTCAAGTTTGATGTTCATATTGAT 1644

Qy        482 AlaAspGluAspAspLeuAlaValIleSerProGluAsnAlaGluPheAlaGlySerPhe 501
Db       1645 GATGATGAAGACAATTTGAGT------GGTCCGGATGAGACAGAGTTTGTGGGAAGTTTT 1698

Qy        502 ValSerLeuTrpHisLysProIleLysGlyLysArgThrLysThrGlnLeuLeuThrLeu 521
Db       1699 GTGAATGTGCAGCATGGG------CATGGCCATAATGTCAAAACTAGC---TTTAAGGTA 1749

Qy        522 SerIleCysAspIleLeuGluAspLeuAspAlaAspGluAspAspTyrValLeuValThr 541
Db       1750 GGGATATCGAAAGTGCTGGAGAGTGTAGAAGCTGAAGAAGACGATGAGGTGCTGGTTTCT 1809

Qy        542 LeuValProArg---AsnAlaGlyAspAlaIleLysIleHisAsnValLysIleGlu 559
Db       1810 TTGGTACCTAAGGTGGGAAAAGGGGATGCCATA---ATAGGAGGCATCAAAATTGAG 1863

RESULT 7
US-09-889-463A-13
; Sequence 13, Application US/09889463A
; Patent No. 6680185
```

```
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
;   LENGTH: 1993
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-889-463A-13

Alignment Scores:
Pred. No.:                9.42e-144      Length:          1993
Score:                    1292.00        Matches:         260
Percent Similarity:       64.52%         Conservative:    80
Best Local Similarity:    49.34%         Mismatches:      161
Query Match:              43.20%         Indels:          26
DB:                       4              Gaps:            10

US-09-446-089E-2 (1-562) x US-09-889-463A-13 (1-1993)

Qy         39 LeuLeuIleValGlyLeuTyrIleAlaAsnSerLeuAlaTyrAlaArgPheAlaSerThr 58
Db        183 CTCCTCGGCCTCGGCAGCGCCGCGGCGGCCGGGCTGGGCGCGCAGCGGGCCCGAGGGGCG 242

Qy         59 SerThrGlyProIleAlaAlaProAspValThrLysCysGlyGlnProAspLeuProPro 78
Db        243 ATTGCCGCGCCCATCCAGGCCCCGGACCTCGGCAACTGCAACCCGCCCGACCTC---CCG 299

Qy         79 GlyThrAlaPro---IleAsnCysCysProProIleProAlaLysIleIleAspPheGlu 97
Db        300 AACACGGCGCCTGACACCAACTGCTGCCCGACGTCCGGCACCGGCATCATCGACTTCGTG 359

Qy         98 LeuProProProSerThrThr---MetArgValArgArgAlaAlaHisLeuValAspAsp 116
Db        360 CTGCCGCCGGCCTCCTCGGCGCCGCTCCGCGTGCGCCCGGCCGCGCACCTGGCAGACGCG 419

Qy        117 AlaTyrIleAlaLysPheLysLysAlaValGluLeuMetArgAlaLeuProGluAspAsp 136
Db        420 GAGTACCTGGCCAAGTACGAGCGGGCCGTGGCGCTCATGAAGCAGCTGCCCGCCGACGAC 479

Qy        137 ProArgSerPheLysGlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyrAsn 156
Db        480 CCGCGCAGCTTCGAGCAGCAGTGGCGCGTGCACTGCGCCTACTGCGACGGCGCCTACGAC 539

Qy        157 GlnAlaGlyPheThrAsnLeuLysLeuGlnIleHisArgSerTrpLeuProPheProPhe 176
Db        540 CAGGTCGGCTTCCCGGACCTGGAGATCCAGGTGCACAACTGCTGGCTCTTCTTCCCATGG 599

Qy        177 HisArgTyrTyrIleTyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThrThr 196
Db        600 CACAGGTTCTACCTCTACTTCCACGAGCGGATCCTCGGCAAGCTCATCGGCGACGACACC 659

Qy        197 PheAlaLeuGlnPheTrpAsnTyrAspSerProGlyGlyMetThrIleProSerMetPhe 216
Db        660 TTCGCGCTGCCCTTCTGGAACTGGGACGCGCCGGACGGCATGACGCTGCCGGCGATCTAC 719

Qy        217 IleAspThrAsnSerSerLeuTyrAspSerLeuArgAspSerAsnHisGlnProProThr 236
Db        720 GCCAACAGGTCGTCGCCGCTCTACAACGAGAGGCGCAACCCCGCCCACCAGCCGCCGTTC 779

Qy        237 IleValAspLeuAsnTyrAlaPheSerAspSerAspAsnThrThrThrProGluGluGln 256
Db        780 CCGGTCGACCTCGAC------TTCAACGAGATAGATGTCATCATCCCAACAGACGAGCAG 833

Qy        257 MetIleIleAsnLeuLysIleValTyrArgGlnMetValSerSerAlaLysThrProGln 276
Db        834 ATCGACCAGAACCTCAACATCATGTACCGCCAGATGGTGTCGGGTGCCAAGAAGACTCGG 893

Qy        277 LeuPhePheGlyArgProTyrArgArgGlyAspGlnGluPheProGlyValGlySerIle 296
Db        894 CTGTTCATGGGGCAGCCGTACCGCGCCGGCGACCAGCCGGACCCTGGCGCGGGCTCCGTG 953

Qy        297 GluLeuValProHisGlyMetIleHisLeuTrpThrGlySerGluAsnThrProTyrGly 316
Db        954 GAGAACGTGCCGCACGGCACGATGCACACCTGGACGGGCGACCCGGCGCAACCCAACAAC 1013

Qy        317 GluAsnMetGlyAlaPheTyrSerThrAlaArgAspProIlePhePheAlaHisHisSer 336
Db       1014 GAGGACATGGGCAACTTCTACTCGGCGGCGCGCGACCCCATCTTCTTCGCGCACCACGGC 1073

Qy        337 AsnValAspArgMetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThrAspLeu 356
Db       1074 AACATCGACCGCCTCTGGCACGTCTGGCGCGGCCTC---CGCCCCGGCAACGCCGACTTC 1130

Qy        357 ThrAspProAspPheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGluMetVal 376
Db       1131 ACCGACACTGACTGGCTTGACACCGCCTTCCTCTTCTACGACGAGGAGGCCCGCCCCGTG 1190

Qy        377 ArgValLysValArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGlnAspVal 396
Db       1191 CGCGTCCGCGTCCGCGACTGCCTCGACCCGGCCGCCATGGGGTACGCGTACCAGGACGTC 1250

Qy        397 GluIleProTrpLeuAsnThrArgProThrProLysValSerProSerLeuLeuLysLys 416
Db       1251 GGCCTGCCGTGGCTGAAAGCCAAGCCGGCC--------------------------AAG 1283

Qy        417 PheHisArgThrAsnThrAlaAsnProArgGlnValPheProAlaIleLeuAspArgVal 436
Db       1284 AGATCCCGCAGGACGCCGGCGCCCGCCGCGGGCGCGCTCCCGGCGACGCTGAGGGAGACC 1343

Qy        437 LeuLysValIleValThrArgProLysLysThrArgSerArgLysGluLysAspGluLeu 456
Db       1344 GTGCGGGTGACGGTGACAAGGCCCCAGGTGTCGAGGAGCGACAAGGAGAAGGAGGAGGCG 1403

Qy        457 GluGluIleLeuValIleGluGlyIleGluLeuGluArgAspHisGlyHisValLysPhe 476
Db       1404 GAGGAGGTGCTGATCGTCGAGGGGATCCAGGTCGCCGACCACTTCAAGTTCGTCAAGTTC 1463

Qy        477 AspValTyrIleAsnAlaAspGluAsp------AspLeuAlaValIleSerProGluAsn 494
Db       1464 GACGTGCTGGTGAACGCGCCCGAGAGCGGAGGCGATGCCGCG--------------TCG 1508

Qy        495 AlaGluPheAlaGlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThr 514
Db       1509 GGGTACTGCGCCGGCAGC---GTCGCGATGACGCCGCACATGGTCCGGACGAACAAGAAG 1565

Qy        515 LysThrGlnLeuLeuThrLeuSer---------IleCysAspIleLeuGluAspLeuAsp 531
Db       1566 AAGGGCTCCGTGAAGACGGTGGCGAGGTTCGGCGTCTGCGACCTGATGGACAACATCGGG 1625

Qy        532 AlaAspGluAspAspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIle 551
Db       1626 GCAGACGGCGACAAGACGGTGGTCGTGTCGCTTGTGCCCAGGTGCGGCGGCGAGCTGGTC 1685

Qy        552 LysIleHisAsnValLysIle 558
Db       1686 ACCATCGGCGGCGTCAGCATC 1706

RESULT 8
US-09-889-463A-31
; Sequence 31, Application US/09889463A
; Patent No. 6680185
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT:  Falco, Saverio C.
;  APPLICANT:  Kinney, Anthony J.
;  APPLICANT:  Miao, Guo-Hua
```

```
;  TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs
;  FILE REFERENCE: BB1330
;  CURRENT APPLICATION NUMBER: US/09/889,463A
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 60/119,590
;  PRIOR FILING DATE: 1999-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
;   LENGTH: 1994
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-889-463A-31

Alignment Scores:
Pred. No.:                3.32e-139      Length:          1994
Score:                    1254.00        Matches:         270
Percent Similarity:       61.45%         Conservative:    87
Best Local Similarity:    46.47%         Mismatches:      178
Query Match:              41.93%         Indels:          46
DB:                       4              Gaps:            17

US-09-446-089E-2 (1-562) x US-09-889-463A-31 (1-1994)

Qy          11 LysLeuSerSerLysSerAsnAspAsn----------------------AspGlnGlu 22
               |||:::|||      ||||||  |||                      ::::::
Db         175 AAAGTGTCATGCAACAGTAACCAAAACACCCCAACACCAAACCCAGAAGAAGAAAAACCA 234

Qy          23 SerSerHisArgCys------LysHisIleLeuLeuPheIleIleThrLeuPheLeuLeu 40
               ||||||:::            ||||||                    :::   |||
Db         235 TCGTCATACAACATTCTAGGAAAACATAGGAGG-----------GATATTCTCCTTGGC 282

Qy          41 IleValGlyLeuTyrIleAlaAsnSerLeuAlaTyrAlaArgPheAlaSerThrSerThr 60
               |||   |||||||||   |||::::::|||:::                :::   :::
Db         283 ATTGGGGGCCTTTACGGTGCTTCTGCTCTTAGCAACACCAACCCTTTAGCCATGGCTGCA 342

Qy          61 GlyProIleAlaAlaProAspValThrLysCysGly---GlnProAspLeuProProGly 79
               ||||||     ||||||:::      |||          |||:::|||   |||
Db         343 GCTCCTATTCTAGAGCCTGACCTAGAACATTGTTGTATAACTGATGATGTACCTAAAGGG 402

Qy          80 ------ThrAlaProIleAsnCysCysProPro---IleProAlaLysIleIleAspPhe 96
                     :::   ||||||||||||         :::      |||||||||
Db         403 GAAATCGAGAAACAAGTCTATTGTTGCCCACCAAAATCTTCTTCCCCTCCTATAGATTTC 462

Qy          97 GluLeuProProProSerThrThrMetArgValArgArgAlaAlaHisLeuValAspAsp 116
               :::|||   |||      |||   :::||||||||        |||      |||   |||
Db         463 AAGTTG---CCTAAAGGAACACCCCTTAGGGTTAGACCACCTGCTCAATTTGTGACCGAT 519

Qy         117 AlaTyrIleAlaLysPheLysLysAlaValGluLeuMetArgAlaLeuProGluAspAsp 136
               |||:::   |||:::|||   |||::::::   ||||||   ||||||   ||||||
Db         520 GAGTACCTAGAAAAGTATAAGTTAGCCCTTAAGCGCATGAGAGAGCTTCCATCTGATGAT 579

Qy         137 ProArgSerPheLysGlnGlnAlaAsnValHisCysAlaTyrCysAlaGlyAlaTyrAsn 156
               ||||||||||||||||||||||||:::::|||||||||||||||   |||   |||
Db         580 CCTCGAAGTTTCAAGCAACAAGCTGATATCCATTGTGCTTATTGTGATGGTGGCTATAAG 639

Qy         157 GlnAlaGlyPhe---ThrAsnLeuLysLeuGlnIleHisArgSerTrpLeuPhePhePro 175
               |||   ||||||      |||      ::::::|||   ||||||:::|||||||||
Db         640 CAATTAGGGTTCCCAGTTGAGCTAGACTTCAAAGTCCACTTTTCATGGATATTTTTCCCT 699

Qy         176 PheHisArgTyrTyrIleTyrPhePheGluArgIleLeuGlyLysLeuIleAsnAspThr 195
               |||||||||:::|||:::||||||:::|||||||||||||||   ||||||:::|||
Db         700 TTCCACCGTTGGTACCTCTATTTCTATGAGCGAATCTTGGGTAGCTTGATTGATGACCCA 759

Qy         196 ThrPheAlaLeuGlnPheTrpAsnTyrAspSerPro---GlyGlyMetThrIleProSer 214
               ||||||||||||   :::||||||:::|||:::|||   |||||||||   :::||||||
Db         760 ACCTTTGCACTTCCATATTGGAACTGGGACAATCCTGATGGTGGCATGGTATTGCCTTCC 819

Qy         215 MetPheIleAspThrAsnSerSerLeuTyrAspSerLeuArgAspSerAsnHisGlnPro 234
               :::|||   |||   :::|||   |||||||||      |||:::   :::      |||
Db         820 ATTTTCGCAGATGAAGACTCCCCTCTATATGACCCTCGCAGGAATCCAGACATCACACCA 879

Qy         235 ProThrIleValAspLeuAsnTyrAlaPheSerAspSerAspAsnThrThrThrProGlu 254
               |||:::||||||||||||||||                        :::      |||
Db         880 ACTACTCTCGTAGACCTAAACTATGGC--------------------AGTGGAAAGGAA 918

Qy         255 GluGlnMetIleIleAsnLeuLysIleValTyrArgGlnMetValSerSerAlaLysThr 274
                     :::      ||||||  ::::::|||     :::|||||||  ||||||
Db         919 CCAAGCGTAGAACAAAACCTCGGTGTAATGTATACGAGTGTTGTCTCTGGTGCGAAACGC 978

Qy         275 ProGlnLeuPhePheGlyArgProTyrArgArgGlyAspGlnGluPheProGlyValGly 294
               ||||||   |||:::|||:::      |||   |||                   |||
Db         979 GCATCGCTCTTCCATGGAAAACCATTTCTTGCTGGAAAGCAGCCTGAGCTAAGTGGAGGG 1038

Qy         295 SerIleGluLeuValProHisGlyMetIleHisLeuTrpThrGlySerGluAsnThrPro 314
               ::::::||||||   ||||||      :::|||   |||||||||            |||
Db        1039 ACCGTAGAGCTTGGTCCTCATACTGCTGTCCACCGTTGGACCGGTGATCCAAGACAACCT 1098

Qy         315 TyrGlyGluAsnMetGlyAlaPheTyrSerThrAlaArgAspProIlePhePheAlaHis 334
               |||:::||||||   |||||||||      |||||||||   |||::::::|||
Db        1099 AACAAAGAGGACATGGGGAGGTTCTATTCTGCTGGAAGAGACCCCGCTTTCTATTCTCAC 1158

Qy         335 HisSerAsnValAspArgMetTrpSerIleTrpLysThrLeuGlyGlyProArgArgThr 354
               |||:::|||||||||||||||||:::|||||||||||||:::          :::|||
Db        1159 CATGCCAACGTGGATCGTATGTGGAATATATGGAAAACAATACCAAGTGGAAAAAGAAGG 1218

Qy         355 AspLeuThrAspProAspPheLeuAspAlaSerPheValPheTyrAspGluAsnAlaGlu 374
               |||      :::   |||:::|||:::   ||||||   ||||||||||||||||
Db        1219 GATTTCAAAAACCGTGATTGGTTGGAAACCTCCTTTTCTTCTACGATGAGAACAAGACC 1278

Qy         375 MetValArgValLysValArgAspCysLeuAspGluLysLysLeuGlyTyrValTyrGln 394
               :::|||||||||||||||:::|||   ||||||      |||:::|||||||||||||
Db        1279 CTTGTCCGTGTGAAGGTGAAAGACAGCCTTGACACGAATAAGATGGGTTATGTTTACCAA 1338

Qy         395 AspValGluIleProTrpLeuAsnThrArgProThrProLysValSerProSerLeuLeu 414
               ||||||   ||||||||||||      :::|||   ||||||   :::
Db        1339 GATGTCGCCATTCCATGGCTCGAGAAAAAGCCTAAACCCAAAAGAACTAGAAAGGCTAAG 1398

Qy         415 Lys--------------LysPheHisArgThrAsnThrAla--------------Asn 424
               |||              :::|||          |||                  |||
Db        1399 AAGGTGGCGTTCGCACAACAATTTGGCGGCATTGGTGCAGCAATGGCTGCTGAGACTGGG 1458

Qy         425 ProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThrArg 443
               |||          ||||||      :::||||||      :::   ::::::|||   |||
Db        1459 CCAAGTTCCAAGTTTCCTCTCACTTTGTTGGACTCAAAGGTAACCCTACTAGTTAAAAGG 1518

Qy         444 ProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIleGlu 463
               ||||||:::   ||||||:::::::::|||:::|||   ||||||:::|||||||:::
Db        1519 CCAAAGCAGTTGAGGAGCAAGAGGGACAAGGAGGAAGAGGAAGAAGTGTTGGTGATTGAT 1578

Qy         464 GlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAlaAsp 483
               |||||||||   :::   |||   ||||||||||||||||||||
Db        1579 GGGATTGAGTTTGATGGGGAT---GATGATGTGAAGTTTGATGTCTATATTACT------ 1629

Qy         484 GluAspAspLeuAlaValIleSerProGluAsnAlaGluPheAlaGlySerPheValSer 503
               ::::::|||:::      |||   |||||||::   ||||||||||||||||||   :::
Db        1630 GATGAAGATGTCGAGGATATTGGACCAGAGAGCACAGAGTTTGCAGGAAGCTTTTCGACT 1689

Qy         504 LeuTrpHisLysProIleLys---------GlyLysArgThrLysThrGlnLeuLeuThr 520
               |||   |||                     |||:::   ||||||      ||||||
Db        1690 CTGGGTCATTCCCATTCGAACATGAACATGGACAAGAAGATCAAAACTAGC---TTGACA 1746

Qy         521 LeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAspAspTyrValLeuVal 540
               |||   |||   |||:::|||||||||||||||||::   ||||||   |||||||||
Db        1747 CTGGGAATAACAGATTTGTTAGAGGACTTGGATGCTGAAAATGATGATAGTGTTTTGGTC 1806

Qy         541 ThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsnValLysIleGluLeu 560
               ||||||||||||||:::          |||   |||   |||:::|||||||||
Db        1807 ACATTGGTACCACGATCTGAGAATGTAACCATCACAATCCAGAACATAAAGATAGAGTTT 1866

Qy         561 Asp 561
               :::
Db        1867 GAG 1869

RESULT 9
US-09-443-067-25
```

```
; Sequence 25, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
;  APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
;  APPLICANT: ORGANISATION
;  TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
;  TITLE OF INVENTION: pineapple
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/443,067
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: US 08/976, 222
;  EARLIER FILING DATE: 1997-11-21
;  EARLIER APPLICATION NUMBER: PCT/AU98/00362
;  EARLIER FILING DATE: 1998-05-19
;  EARLIER APPLICATION NUMBER: AU PP3898
;  EARLIER FILING DATE: 1995-05-23
;  EARLIER APPLICATION NUMBER: AU PP6849
;  EARLIER FILING DATE: 1997-05-19
;  EARLIER APPLICATION NUMBER: AU PP5600
;  EARLIER FILING DATE: 1995-09-26
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1522
;   TYPE: DNA
;   ORGANISM: pineapple
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)..(1271)
US-09-443-067-25

Alignment Scores:
Pred. No.:                8.64e-138      Length:          1522
Score:                    1240.50        Matches:         233
Percent Similarity:       71.13%         Conservative:    70
Best Local Similarity:    54.69%         Mismatches:      104
Query Match:              41.47%         Indels:          19
DB:                       4              Gaps:            6

US-09-446-089E-2 (1-562) x US-09-443-067-25 (1-1522)

Qy        147 HisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeuGln 166
              ||||||||||||||   |||||||||:::|||   ||||||   :::|||:::::::|||
Db          3 CACTGTGCGTATTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCCAG 62

Qy        167 IleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGluArg 186
              ||||||   ||||||||||||||||||:::||||||:::|||:::|||      ||||||
Db         63 ATCCACAACTCGTGGCTCTTCTTTCCTTGGCACCGGTTCTACCTCTACTCCAACGAGCGC 122

Qy        187 IleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAspSer 206
              ||||||||||||||||||   |||   ||||||||||||   |||||||||:::|||:::
Db        123 ATACTCGGGAAACTTATCGGCGACGACACGTTCGCGCTGCCTTTCTGGAACTGGGACGCG 182

Qy        207 ProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAspSer 226
              ||||||||||||      ||||||::::::   |||   :::|||||||||||||||||
Db        183 CCGGGGGGCATGCAGTTCCCGTCTATCTACACGGACCCTTCATCCTCGCTATATGACAAG 242

Qy        227 LeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSerAsp 246
              |||||||||:::   ||||||||||||||||:::::::|||||||:::|||      :::
Db        243 CTGCGTGATGCGAAGCACCAGCCGCCGACTTTGATTGACCTCGACTAC------AATGGC 296

Qy        247 SerAspAsnThrThrThrProGluGluGlnMetIleIleAsnLeuLysIleValTyrArg 266
              :::|||   |||   :::||||||||||||:::      ||||||   ::::::||||||
Db        297 ACCGATCCTACCTTCTCCCCTGAAGAACAGATTAACCACAACCTCGCCGTCATGTACCGA 356

Qy        267 GlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArgArgGly 286
              |||::::::||||||   ||||||||||:::||||||   |||      ||||||   |||
Db        357 CAGGTGATATCCAGTGGAAAGACACCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGT 416

Qy        287 AspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIleHisLeu 306
              ||||||      ||||||   ||||||:::|||      |||||||||   :::|||:::
Db        417 GACCAGCCTGACCCCGGCGCAGGCTCTGTAGAGCAGAAGCCGCACGGCCCGGTGCATGTG 476

Qy        307 TrpThrGlySerGluAsnThrProTyrGlyGluAsnMetGlyAlaPheTyrSerThrAla 326
              ||||||||      |||   |||      |||:::||||||      ||||||   |||
Db        477 TGGACAGGTGATCGCAACCAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGGCG 536

Qy        327 ArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSerIleTrpLys 346
              ||||||:::|||||||||||||||   |||:::||||||||||   :::|||:::
Db        537 TGGGACCCCGTCTTCTTCGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGG 596

Qy        347 ThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAspAlaSerPhe 366
              |||||||||      |||   :::   ||||||||||||:::|||:::|||||||||
Db        597 AACCTTGGCGGCAAGCACCGC---AACTTCACCGACCCCGACTGGCTCAACGCGTCCTTC 653

Qy        367 ValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCysLeuAspGlu 386
              :::|||||||||||||||||:::::|||||||||||||:::||||||||:::
Db        654 CTGTTCTATGATGAGAATGCGCAGCTCGTCCGTGTTAAAGTAAAAGACTGCTTAGAGGCC 713

Qy        387 LysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThrArgProThr 406
                  :::   |||   |||||||||||||||||||||||||||      :::|||||||
Db        714 GACGCAATGCGGTACACATACCAGGATGTAGAGATCCCGTGGCTCAAAGCAAAGCCGACG 773

Qy        407 ProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAlaAsnProArg 426
              ||||||   :::         :::|||              |||      |||   ||||||
Db        774 CCAAAGAGCGCCCTACAGAAGATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGG 833

Qy        427 ----------------------GlnValProProAlaIleLeuAspArgValLeuLys 438
                                     ||||||   :::|||||:::   :::
Db        834 GGGACGACGACTACCACAGCAGAGACTACATTTCCGGTGGTGCTGGATAAGCCGGTGAGT 893

Qy        439 ValIleValThrArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGlu 458
                  |||   |||||||||      ||||||   |||||||||:::|||   ||||||
Db        894 GCAACAGTGGCTAGACCGAAGGCCAGGAGGAGTGGGAAGGAGAAGGAAGAAGAGGAGGAG 953

Qy        459 IleLeuValIleGluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspVal 478
              :::||||||:::|||||||||||||||||||:::|||          ||||||||||||||
Db        954 GTGTTGGTGGTGGAGGGAATCGAGTTGGAGAAGGAC---GTGTTCGTGAAGTTTGATGTG 1010

Qy        479 TyrIleAsnAlaAspGluAspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
              |||||||||:::   |||   :::         :::   ||||||   :::||||||||||
Db       1011 TATATAAACTCGCCGGAGCACGAA------GGGGTGGGGCCGGAGGCGAGTGAGTTCGCA 1064

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLysThrGlnLeu 518
              ||||||||||||   :::   ||||||      |||   |||:::   |||
Db       1065 GGGAGCTTCGTCCACGTGCCACACAAGCACAAGAAGGCGAAGAAGGGGAAGGAGATGGCC 1124

Qy        519 ---------------LeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAsp 533
                              |||   |||   |||   |||:::|||||||||:::   |||:::
Db       1125 AGGATGAACACAAGGCTTAAGCTCGGGATAACGGACCTGCTCGAGGACATCGGCGCTGAG 1184

Qy        534 GluAspAspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIle 553
              :::|||:::   ||||||:::|||||||||||||:::           :::|||:::
Db       1185 GACGACGAGAGCGTGCTCATCACGCTCGTGCCCAGGAGCGGCAAGGGAATGGTGAAGGTT 1244

Qy        554 HisAsnValLysIleGlu 559
                    ::::::|||:::
Db       1245 GGAGGGCTAAGGATTGAT 1262

RESULT 10
US-08-481-190-1
; Sequence 1, Application US/08481190
; Patent No. 6160204
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNA
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticutt
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
```

```
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,190
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  203,533
;      FILING DATE:  02-24-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  UA 816 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1761 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-481-190-1

Alignment Scores:
Pred. No.:                4.12e-128      Length:          1761
Score:                    1160.50        Matches:         249
Percent Similarity:       60.60%         Conservative:    94
Best Local Similarity:    43.99%         Mismatches:      180
Query Match:              38.80%         Indels:          43
DB:                       3              Gaps:            17

US-09-446-089E-2 (1-562) x US-08-481-190-1 (1-1761)

Qy         11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30
              |||:::|||     :::|||:::   |||:::             :::
Db        142 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 201

Qy         31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50
              :::|||                  |||   :::   |||||||||   |||   :::|||
Db        202 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 243

Qy         51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70
              |||                  :::     ||||||     |||||:::
Db        244 GCA------------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 291

Qy         71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89
              ||||||        :::     |||         |||   :::|||||||||||:::
Db        292 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 351

Qy         90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107
              |||   :::|||      :::   :::          |||      |||   :::|||:::
Db        352 CCCGATGAGATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 411

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
              |||     ||||||     |||:::   |||:::||||||::::::   |||
Db        412 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 471

Qy        128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145
                 ||||||   |||   :::|||      ||||||     ||||||||||||||||||
Db        472 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 531

Qy        146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165
              :::|||||||||||||||   |||||||||          |||            :::|||
Db        532 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGT---------AAAGAATTG 582

Qy        166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185
              |||:::|||   |||||||||||||||||||||||||:::|||:::|||||:::|||
Db        583 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 642

Qy        186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205
              |||||||||||   |||||||||||   |||||||||||   :::||||||:::|||
Db        643 AGAATTTTGGGATCACTTATTAATGATCCAACTTTTGCTTTACCTTACTGGAATTGGGAT 702

Qy        206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225
              |||   ||||||   ||||||   ||||||              ||||||||||||||||
Db        703 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 762

Qy        226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245
              |||:::   ||||||:::      ||||||:::||||||   :::
Db        763 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 822

Qy        246 AspSerAspAsnThrThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264
              :::   |||          ||||||:::   |||   |||      ||||||   ::::::
Db        823 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 873

Qy        265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284
              ||||||||||||||:::::|||      |||      |||||||||      |||
Db        874 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCCT 933

Qy        285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
              |||   ::      ||||||   |||:::||||||   :::||||||      :::
Db        934 CTGGGTTCTGAACCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 993

Qy        305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323
              |||:::|||||||   :::      ||||||:::||||||   ||||||
Db        994 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1053

Qy        324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343
              |||          ||||||||||||:::   ||||||:::||||||||||||||||:::
Db       1054 TCACCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1113

Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363
              ||||||   :::||||||   ||||||   ||||||||||||   |||:::|||:::
Db       1114 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1170

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383
              :::   |||  ||||||||||||||||||          |||||||||      ||||||
Db       1171 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAGTCCGTAGACTGT 1230

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403
              ||||||   ||||||:::|||:::   |||      :::      ||||||   |||
Db       1231 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1290

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423
              :::|||      |||   |||                 |||   :::      :::   |||
Db       1291 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1341

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442
                 :::||||||||   |||   |||||||||   :::          :::|||
Db       1342 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1401

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462
              ||||||      :::|||:::   :::||||||:::|||   ||||||||||||
Db       1402 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAAGAGGAGATACTGACATTC 1461

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482
              |||      :::   |||      :::|||:::|||||||||:::::|||
Db       1462 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1518

Qy        483 AspGlu-----------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
              |||:::             |||:::|||          :::   ||||||||||||
Db       1519 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1563

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys--------- 515
              ||||||:::   ||||||   |||      :::   |||      |||
Db       1564 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1617

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535
              :::            |||:::|||   ::::::|||||||||:::      ::::::::
Db       1618 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1677

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555
              |||   :::   ||||||||||||||:::      |||:::   :::   |||   :::
```

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Db       1678 GATACTATTGCGGTGACTTTGGTTCCAAAAGCTGGCGGTGAAGAAGTGTCCATTGAAAGT 1737

Qy        556 ValLysIleGluLeuAsp 561
              |||:::|||:::|||:::
Db       1738 GTGGAGATCAAGCTTGAG 1755

RESULT 11
PCT-US93-00869-1
; Sequence 1, Application PC/TUS9300869
;  GENERAL INFORMATION:
;    APPLICANT:  John C. Steffens
;    TITLE OF INVENTION:  Polyphenol Oxidase cDNAs: Cloning
;    TITLE OF INVENTION:  and Applications
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00869
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  CRF D-1057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1761 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US93-00869-1

Alignment Scores:
Pred. No.:                4.12e-128       Length:          1761
Score:                    1160.50         Matches:         249
Percent Similarity:       60.60%          Conservative:    94
Best Local Similarity:    43.99%          Mismatches:      180
Query Match:              38.80%          Indels:          43
DB:                       5               Gaps:            17

US-09-446-089E-2 (1-562) x PCT-US93-00869-1 (1-1761)

Qy         11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30
              |||:::|||     :::|||:::   |||:::           :::
Db        142 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 201

Qy         31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50
              :::|||                 |||   :::   |||||||||   |||   :::|||
Db        202 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 243

Qy         51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70
              |||                    :::     ||||||     ||||||:::
Db        244 GCA------------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 291

Qy         71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89
              ||||||          :::      |||          |||   :::|||||||||||:::
Db        292 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 351

Qy         90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107
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              |||   :::|||      :::   :::         |||      |||   :::|||:::
Db        352 CCCGATGAGATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 411

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
              |||     ||||||     |||:::   |||:::||||||::::::   |||
Db        412 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 471

Qy        128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145
              ||||||   |||   :::|||      ||||||      |||||||||||||||||||
Db        472 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 531

Qy        146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165
              :::||||||||||||||   ||||||||        |||          :::|||
Db        532 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGT---------AAAGAATTG 582

Qy        166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185
              |||:::|||   |||||||||||||||||||||||||:::|||:::||||||:::|||
Db        583 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 642

Qy        186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205
              ||||||||||||   ||||||||||||   ||||||||||||   :::||||||:::|||
Db        643 AGAATTTTGGGATCACTTATTAATGATCCAACTTTTGCTTTACCTTACTGGAATTGGGAT 702

Qy        206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225
              |||   ||||||   ||||||   ||||||                ||||||||||||||
Db        703 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 762

Qy        226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245
                  |||:::   ||||||:::      ||||||:::|||||   :::
Db        763 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 822

Qy        246 AspSerAspAsnThrThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264
              :::   |||         ||||||:::   |||   |||      ||||||   ::::::
Db        823 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 873

Qy        265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284
              |||||||||||||||:::::|||       |||       |||||||||       |||
Db        874 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCCT 933

Qy        285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
                 |||   :::      ||||||   |||:::||||||   :::||||||      :::
Db        934 CTGGGTTCTGAACCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 993

Qy        305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323
              |||:::||||||||   :::            ||||||:::||||||   ||||||
Db        994 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1053

Qy        324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343
              |||          ||||||||||||:::   ||||||:::||||||||||||||||:::
Db       1054 TCACCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1113

Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363
              ||||||   :::||||||   ||||||   ||||||||||||   |||:::|||:::
Db       1114 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1170

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383
              :::   |||   ||||||||||||||||              ||||||||    ||||||
Db       1171 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAGTCCGTAGACTGT 1230

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403
              ||||||   ||||||:::|||:::   |||      :::      ||||||   |||
Db       1231 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1290

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423
              :::|||     |||   |||          |||   :::      :::   |||
Db       1291 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1341

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442
                  :::||||||||||   |||   |||||||||   :::          :::|||
Db       1342 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1401

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462
              ||||||      :::|||:::   :::||||||:::|||   ||||||||||||
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Db       1402 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAAGAGGAGATACTGACATTC 1461

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482
                  |||      :::   |||      :::|||:::||||||||:::::|||
Db       1462 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1518

Qy        483 AspGlu-----------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
              |||:::           |||:::|||       :::   ||||||||||
Db       1519 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1563

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys------- 515
              ||||||:::   ||||||   |||      :::   |||       |||
Db       1564 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1617

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535
              :::           |||:::|||   ::::::|||||||:::      :::::::::
Db       1618 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1677

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555
              |||   :::   ||||||||||||||:::      |||:::   :::   |||   :::
Db       1678 GATACTATTGCGGTGACTTTGGTTCCAAAAGCTGGCGGTGAAGAAGTGTCCATTGAAAGT 1737

Qy        556 ValLysIleGluLeuAsp 561
              |||:::|||:::|||:::
Db       1738 GTGGAGATCAAGCTTGAG 1755

RESULT 12
US-09-078-862-1
; Sequence 1, Application US/09078862
; Patent No. 6091003
;  GENERAL INFORMATION:
;    APPLICANT:  Nan, Guo-Ling
;    APPLICANT:  Nagai, Chifumi
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR GENETIC
;    TITLE OF INVENTION:  TRANSFORMATION OF PINEAPPLE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/078,862
;      FILING DATE:  14-MAY-1998
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  UH-03321
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2145 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-078-862-1

Alignment Scores:
Pred. No.:              2.07e-126       Length:         2145
Score:                  1147.50         Matches:        248
Percent Similarity:     60.25%          Conservative:   93
Best Local Similarity:  43.82%          Mismatches:     182

Query Match:            38.37%          Indels:         43
DB:                     3               Gaps:           17

US-09-446-089E-2 (1-562) x US-09-078-862-1 (1-2145)

Qy          11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30
               |||:::|||      :::|||:::  |||:::           :::
Db         256 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 315

Qy          31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50
               :::|||                |||  :::  |||||||||  |||  :::|||
Db         316 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 357

Qy          51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70
               |||                    :::      ||||||      ||||||:::
Db         358 GCA-----------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 405

Qy          71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89
               |||||          :::     |||          |||   :::|||||||||||:::
Db         406 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 465

Qy          90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107
               |||      |||      :::  :::          |||      |||   :::|||:::
Db         466 CCCGATGATATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 525

Qy         108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
               |||      ||||||      |||:::  |||:::||||||::::::  |||
Db         526 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 585

Qy         128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145
                  ||||||  |||   :::|||      ||||||      ||||||||||||||||
Db         586 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 645

Qy         146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165
               :::||||||||||||||    |||||||||          |||           :::|||
Db         646 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGC---------AAAGAATTG 696

Qy         166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185
               |||:::|||   |||||||||||||||||||||||||::|||:::||||||:::|||
Db         697 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 756

Qy         186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205
               ||||||||||  ||||||||||  ||||||||||  :::|||||:::|||
Db         757 AGAATTTTGGGATCACTTATTAATGATCCAACTTTTGCTTTACCTTACTGGAATTGGGAT 816

Qy         206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225
               |||  ||||||  ||||||  ||||||           ||||||||||||||
Db         817 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 876

Qy         226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245
                     |||:::  ||||||:::      ||||||:::|||||  :::
Db         877 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 936

Qy         246 AspSerAspAsnThrThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264
               :::  |||          ||||||:::  |||  |||       ||||||  ::::::
Db         937 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 987

Qy         265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284
               ||||||||||||||:::::|||      |||      ||||||||      |||
Db         988 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCTC 1047

Qy         285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
                              ||||||  |||:::||||||  :::||||||      :::
Db        1048 TGGGTTCTGAACCCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 1107

Qy         305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323
               |||:::||||||||  :::          ||||||:::||||||  ||||||
Db        1108 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1167

Qy         324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343
               |||         ||||||||||:::  ||||||:::||||||||||||||||:::
Db        1168 TCAGCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1227
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Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363
Db       1228 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1284

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383
Db       1285 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAAGTCCGTGATGTT 1344

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403
Db       1345 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1404

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423
Db       1405 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1455

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442
Db       1456 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1515

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462
Db       1516 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAGGAGGAGATTCTGACATTC 1575

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482
Db       1576 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1632

Qy        483 AspGlu------------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
Db       1633 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1677

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys--------- 515
Db       1678 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1731

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535
Db       1732 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1791

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555
Db       1792 GATACTATCGCGGTGACTTTAATTCCAAAAGCTGGCGGTGAAGGTGTATCCATTGAAAGT 1851

Qy        556 ValLysIleGluLeuAsp 561
Db       1852 GTGGAGATCAAGCTTGAG 1869
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RESULT 13
US-09-866-153-11
; Sequence 11, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT:  Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-03648
;  CURRENT APPLICATION NUMBER: US/09/866,153
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 09/270,976
;  PRIOR FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2146
;   TYPE: DNA
;   ORGANISM: Lycopersicon esculentum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)
;   OTHER INFORMATION: The "n" at position 16 is any nucleotide.
US-09-866-153-11
```

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Alignment Scores:
Pred. No.:                2.07e-126      Length:          2146
Score:                    1147.50        Matches:         248
Percent Similarity:       60.25%         Conservative:    93
Best Local Similarity:    43.82%         Mismatches:      182
Query Match:              38.37%         Indels:          43
DB:                       4              Gaps:            17

US-09-446-089E-2 (1-562) x US-09-866-153-11 (1-2146)

Qy         11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30
Db        257 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 316

Qy         31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50
Db        317 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 358

Qy         51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70
Db        359 GCA------------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 406

Qy         71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89
Db        407 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 466

Qy         90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107
Db        467 CCCGATGATATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 526

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
Db        527 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 586

Qy        128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145
Db        587 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 646

Qy        146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165
Db        647 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGC---------AAAGAATTG 697

Qy        166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185
Db        698 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 757

Qy        186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205
Db        758 AGAATTTTGGGATCACTTATTAATGATCCAACTTTGCTTTACCTTACTGGAATTGGGAT 817

Qy        206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225
Db        818 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 877

Qy        226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245
Db        878 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 937

Qy        246 AspSerAspAsnThrThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264
Db        938 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 988

Qy        265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284
Db        989 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCTC 1048

Qy        285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
Db       1049 TGGGTTCTGAACCCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 1108

Qy        305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323
Db       1109 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1168
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Qy        324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343
              |||         |||||||||||||:::   ||||||:::|||||||||||||||||||:::
Db       1169 TCAGCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1228

Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363
              ||||||   :::||||||   ||||||   ||||||||||||   |||:::|||:::
Db       1229 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1285

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383
              :::   |||   ||||||||||||||||          ||||||||||||||||||
Db       1286 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAAGTCCGTGATGTT 1345

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403
              ||||||   ||||||:::|||:::   |||      :::      ||||||   |||
Db       1346 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1405

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423
              :::|||      |||   |||          |||   :::      :::   |||
Db       1406 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1456

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442
                    :::|||||||||   |||   |||||||||   :::         :::|||
Db       1457 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1516

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462
              ||||||      :::|||:::   :::||||||:::|||   ||||||||||
Db       1517 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAGGAGGAGATTCTGACATTC 1576

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482
                    |||      :::   |||      :::|||:::|||||||||:::::|||
Db       1577 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1633

Qy        483 AspGlu-----------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
              |||:::             |||:::|||              :::   ||||||||||||
Db       1634 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1678

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys--------- 515
              |||||||:::   ||||||   |||      :::   |||      |||
Db       1679 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1732

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535
              :::            |||:::|||   :::::::||||||||:::         :::::::::
Db       1733 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1792

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555
              |||   :::   |||||||||:::|||:::      |||:::   :::   |||   :::
Db       1793 GATACTATCGCGGTGACTTTAATTCCAAAAGCTGGCGGTGAAGGTGTATCCATTGAAAGT 1852

Qy        556 ValLysIleGluLeuAsp 561
              |||:::|||:::|||:::
Db       1853 GTGGAGATCAAGCTTGAG 1870

RESULT 14
US-09-693-467A-11
; Sequence 11, Application US/09693467A
; Patent No. 6686513
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT:  Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-04331
;  CURRENT APPLICATION NUMBER: US/09/693,467A
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 09/270,976
;  PRIOR FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2146
;   TYPE: DNA
;   ORGANISM: Lycopersicon esculentum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)
;   OTHER INFORMATION: The "n" at position 16 is any nucleotide.
US-09-693-467A-11

Alignment Scores:
Pred. No.:                2.07e-126      Length:          2146
Score:                    1147.50        Matches:         248
Percent Similarity:       60.25%         Conservative:    93
Best Local Similarity:    43.82%         Mismatches:      182
Query Match:              38.37%         Indels:          43
DB:                       4              Gaps:            17

US-09-446-089E-2 (1-562) x US-09-693-467A-11 (1-2146)

Qy         11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30
              |||:::|||      :::|||:::   |||:::                  :::
Db        257 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 316

Qy         31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50
              :::|||                  |||   :::   |||||||||   |||   :::|||
Db        317 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 358

Qy         51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70
              |||                  :::      ||||||      |||||:::
Db        359 GCA------------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 406

Qy         71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89
              ||||||          :::      |||          |||   :::|||||||||:::
Db        407 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 466

Qy         90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107
              |||      |||      :::   :::          |||      |||   :::|||:::
Db        467 CCCGATGATATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 526

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127
              |||      ||||||      |||:::   |||:::||||||::::::   |||
Db        527 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 586

Qy        128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145
              ||||||   |||   :::|||      ||||||      ||||||||||||||||||
Db        587 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 646

Qy        146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165
              :::||||||||||||||   ||||||||          |||              :::|||
Db        647 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGC---------AAAGAATTG 697

Qy        166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185
              |||:::|||   |||||||||||||||||||||||||:::|||:::|||||||:::|||
Db        698 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 757

Qy        186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205
              ||||||||||||   ||||||||||||   ||||||||||||   :::|||||||:::|||
Db        758 AGAATTTTGGGATCACTTATTAATGATCCAACTTTTGCTTTACCTTACTGGAATTGGGAT 817

Qy        206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225
              |||   ||||||   ||||||   ||||||                ||||||||||||||
Db        818 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 877

Qy        226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245
                 |||:::   ||||||:::      ||||||:::||||||   :::
Db        878 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 937

Qy        246 AspSerAspAsnThrThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264
              :::   |||          ||||||:::   |||   |||      ||||||   ::::::
Db        938 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 988

Qy        265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284
              ||||||||||||||:::::|||      |||      |||||||||      |||
Db        989 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCTC 1048

Qy        285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
                                  ||||||   |||:::||||||   :::||||||      :::
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Db       1049 TGGGTTCTGAACCCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 1108

Qy        305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323

Db       1109 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1168

Qy        324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343

Db       1169 TCAGCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1228

Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363

Db       1229 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1285

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383

Db       1286 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAAGTCCGTGATGTT 1345

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403

Db       1346 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1405

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423

Db       1406 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1456

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442

Db       1457 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1516

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462

Db       1517 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAGGAGGAGATTCTGACATTC 1576

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482

Db       1577 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1633

Qy        483 AspGlu------------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498

Db       1634 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1678

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys--------- 515

Db       1679 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1732

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535

Db       1733 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1792

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555

Db       1793 GATACTATCGCGGTGACTTTAATTCCAAAAGCTGGCGGTGAAGGTGTATCCATTGAAAGT 1852

Qy        556 ValLysIleGluLeuAsp 561

Db       1853 GTGGAGATCAAGCTTGAG 1870

RESULT 15
US-09-270-976-11
; Sequence 11, Application US/09270976A
; Patent No. 6706948
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT: Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-03648
;  CURRENT APPLICATION NUMBER: US/09/270,976A
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2146
;   TYPE: DNA
;   ORGANISM: Lycopersicon esculentum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)
;   OTHER INFORMATION: The "n" at position 16 is any nucleotide.
US-09-270-976-11

Alignment Scores:
Pred. No.:                2.07e-126      Length:          2146
Score:                    1147.50        Matches:         248
Percent Similarity:       60.25%         Conservative:    93
Best Local Similarity:    43.82%         Mismatches:      182
Query Match:              38.37%         Indels:          43
DB:                       4              Gaps:            17

US-09-446-089E-2 (1-562) x US-09-270-976-11 (1-2146)

Qy         11 LysLeuSerSerLysSerAsnAspAsnAspGlnGluSerSerHisArgCysLysHisIle 30

Db        257 AAGGTTTCATGCAACGCAAACAACGTTGACAAAAACCCTGACGCTGTTGATAGACGAAAC 316

Qy         31 LeuLeuPheIleIleThrLeuPheLeuLeuIleValGlyLeuTyrIleAlaAsnSerLeu 50

Db        317 GTTCTT-----------------TTAGGGTTAGGAGGTCTTTATGGTGCAGCTAATCTT 358

Qy         51 AlaTyrAlaArgPheAlaSerThrSerThrGlyProIleAlaAlaProAspValThrLys 70

Db        359 GCA------------CCATTAGCGACTGCTGCACCTATACCACCTCCTGATCTCAAGTCT 406

Qy         71 CysGlyGlnProAspLeuProProGlyThrAlaProIle---AsnCysCysProProIle 89

Db        407 TGTGGTACTGCCCATGTAAAAGAAGGTGTTGATGTAATATACAGTTGTTGCCCTCCTGTA 466

Qy         90 ProAlaLysIle------IleAspPheGluLeuProProProSerThrThrMetArgVal 107

Db        467 CCCGATGATATCGATAGTGTTCCGTACTACAAGTTCCCTTCTATGACTAAACTCCGCATC 526

Qy        108 ArgArgAlaAlaHisLeuValAspAspAlaTyrIleAlaLysPheLysLysAlaValGlu 127

Db        527 CGCCCCCCTGCTCATGCGGCGGATGAGGAGTACGTAGCCAAGTATCAATTGGCTACGAGT 586

Qy        128 LeuMetArgAlaLeuProGluAsp------AspProArgSerPheLysGlnGlnAlaAsn 145

Db        587 CGAATGAGGGAACTTGATAAAGACCCCTTTGACCCTCTTGGCTTTAAACAACAAGCTAAT 646

Qy        146 ValHisCysAlaTyrCysAlaGlyAlaTyrAsnGlnAlaGlyPheThrAsnLeuLysLeu 165

Db        647 ATTCATTGTGCTTATTGCAACGGTGCTTACAAAGTTGGTGGC---------AAAGAATTG 697

Qy        166 GlnIleHisArgSerTrpLeuPhePheProPheHisArgTyrTyrIleTyrPhePheGlu 185

Db        698 CAAGTTCATTTCTCGTGGCTTTTCTTTCCCTTTCATAGATGGTACTTGTACTTTTACGAA 757

Qy        186 ArgIleLeuGlyLysLeuIleAsnAspThrThrPheAlaLeuGlnPheTrpAsnTyrAsp 205

Db        758 AGAATTTTGGGATCACTTATTAATGATCCAACTTTTGCTTTACCTTACTGGAATTGGGAT 817

Qy        206 SerProGlyGlyMetThrIleProSerMetPheIleAspThrAsnSerSerLeuTyrAsp 225

Db        818 CATCCAAAAGGCATGCGTATACCTCCCATGTTTGATCGTGAGGGATCATCTCTTTACGAT 877

Qy        226 SerLeuArgAspSerAsnHisGlnProProThrIleValAspLeuAsnTyrAlaPheSer 245

Db        878 GAGAAACGTAACCAAAATCATCGCAATGGAACTATTATTGATCTTGGTCATTTTGGTAAG 937

Qy        246 AspSerAspAsnThrThrProGluGluGln---MetIleIleAsnLeuLysIleVal 264

Db        938 GAAGTTGAC---------ACACCTCAGCTACAGATAATGACTAATAATTTAACCCTAATG 988

Qy        265 TyrArgGlnMetValSerSerAlaLysThrProGlnLeuPhePheGlyArgProTyrArg 284

Db        989 TACCGTCAAATGGTTACTAATGCTCCTTGCCCTTCCCAATTCTTCGGTGCTGCTTACCTC 1048
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Qy        285 ArgGlyAspGlnGluPheProGlyValGlySerIleGluLeuValProHisGlyMetIle 304
                          ||||||   |||:::||||||   :::||||||      :::
Db       1049 TGGGTTCTGAACCCAAGTCCGGGTCAGGGTACTATTGAAAACATCCCTCATACTCCGGTT 1108

Qy        305 HisLeuTrpThrGlySerGlu---AsnThrProTyrGlyGluAsnMetGlyAlaPheTyr 323
              |||:::|||||||||   :::                ||||||:::||||||   ||||||
Db       1109 CACATCTGGACCGGTGACAAACCTCGTCAAAAAAACGGTGAAGACATGGGTAATTTCTAC 1168

Qy        324 SerThrAlaArgAspProIlePhePheAlaHisHisSerAsnValAspArgMetTrpSer 343
              |||          ||||||||||||:::   ||||||:::||||||||||||||||||:::
Db       1169 TCAGCCGGTTTAGATCCGATTTTTTACTGCCACCATGCCAATGTGGACAGGATGTGGAAT 1228

Qy        344 IleTrpLysThrLeuGlyGlyProArgArgThrAspLeuThrAspProAspPheLeuAsp 363
                 ||||||   :::||||||   ||||||   ||||||||||||   |||:::|||:::
Db       1229 GAATGGAAATTAATTGGCGGGAAAAGAAGG---GATTTAACAGATAAAGATTGGTTGAAC 1285

Qy        364 AlaSerPheValPheTyrAspGluAsnAlaGluMetValArgValLysValArgAspCys 383
              :::   |||   ||||||||||||||||            ||||||||||||||||
Db       1286 TCTGAATTCTTTTTCTACGATGAAAATCGTAACCCTTACCGTGTGAAAGTCCGTGATGTT 1345

Qy        384 LeuAspGluLysLysLeuGlyTyrValTyrGlnAspValGluIleProTrpLeuAsnThr 403
              ||||||   ||||||:::|||:::   |||      :::      ||||||   |||
Db       1346 TTGGACAGTAAAAAAATGGGATTCGATTACGCGCCAATGCCCACTCCATGGCGTAATTTT 1405

Qy        404 ArgProThrProLysValSerProSerLeuLeuLysLysPheHisArgThrAsnThrAla 423
              :::|||      |||   |||                |||   :::      :::   |||
Db       1406 AAACCAATCAGAAAGTCATCATCAGGA---------AAAGTGAATACAGCGTCAATTGCA 1456

Qy        424 AsnProArgGlnValPhePro---AlaIleLeuAspArgValLeuLysValIleValThr 442
                    :::|||||||||   |||   ||||||||   :::          :::|||
Db       1457 CCAGTTAGCAAGGTGTTCCCATTGGCGAAGCTGGACCGTGCGATTTCGTTCTCTATCACG 1516

Qy        443 ArgProLysLysThrArgSerArgLysGluLysAspGluLeuGluGluIleLeuValIle 462
              ||||||      :::|||:::   :::||||||:::|||   ||||||||||||
Db       1517 CGGCCAGCCTCGTCAAGGACAACACAAGAGAAAAATGAGCAGGAGGAGATTCTGACATTC 1576

Qy        463 GluGlyIleGluLeuGluArgAspHisGlyHisValLysPheAspValTyrIleAsnAla 482
                    |||      :::   |||      :::|||:::||||||||||::::::|||
Db       1577 AATAAAATATCGTATGAT---GATAGGAACTATGTAAGGTTCGATGTGTTTCTGAACGTG 1633

Qy        483 AspGlu-----------AspAspLeuAlaValIleSerProGluAsnAlaGluPheAla 498
              |||:::            |||:::|||          :::   ||||||||||||
Db       1634 GACAAGACTGTGAATGCAGATGAGCTT--------------GATAAGGCGGAGTTTGCA 1678

Qy        499 GlySerPheValSerLeuTrpHisLysProIleLysGlyLysArgThrLys--------- 515
              ||||||:::   ||||||   |||      :::   |||      |||
Db       1679 GGGAGTTATACTAGCTTGCCGCAT------GTTCATGGAAGTAATACTAATCATGTTACC 1732

Qy        516 ThrGlnLeuLeuThrLeuSerIleCysAspIleLeuGluAspLeuAspAlaAspGluAsp 535
              :::            |||:::|||   ::::::||||||||:::      :::::::::
Db       1733 AGTGTTACTTTCAAGCTGGCGATAACTGAACTGTTGGAGGATATTGGATTGGAAGATGAA 1792

Qy        536 AspTyrValLeuValThrLeuValProArgAsnAlaGlyAspAlaIleLysIleHisAsn 555
              |||   :::   |||||||||:::|||:::      |||:::   :::   |||   :::
Db       1793 GATACTATCGCGGTGACTTTAATTCCAAAAGCTGGCGGTGAAGGTGTATCCATTGAAAGT 1852

Qy        556 ValLysIleGluLeuAsp 561
              |||:::|||:::|||:::
Db       1853 GTGGAGATCAAGCTTGAG 1870


Search completed: April  8, 2005, 21:50:13
Job time : 316 secs
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